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Maximum DB
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A Geneseq_21:*
1: geneseqp1980
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Gapop 10.0 ,
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956
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Listing
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Copyright (c) 1993 - 2006 Compugen Ltd
geneseqp2004s:*
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(without alignments)
563.979 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	0	ហ	4	ω	N	–	Result No.
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Add25/65 Hullian Con	Human	Human	Ada43043 Human con	Abr43135 Human con	Abr92069 Human cer	Abp68624 Human pan	Human	Aab48831 Human con	Aab60664 Human con	Aab90791 Human she	Amino	Human	Aay92940 Human con	Aay92939 Human con	Aay18361 Human con	Aaw81425 Connectiv	Aaw62084 Human con	Human	Aaw11302 Connectiv		Abb09204 Human ctg	Conne	Aay92941 Human con	Description

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Adh10252 Rat CTGF	Rat	_	Abr43137 Porcine c		Aea00218 CTGF prot		Human	Human	Human	_	Human	Human	_				Human	_		-

ALIGNMENTS

Human connective tissue growth factor protein fragment.

08-NOV-2000

(first entry)

AAY92941 standard; protein; 172 AA

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RESULT 1
AAY92941
JID AAY92
AXX AAY92
AXX AAY9
AXX AAY9
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XXX 22-J
XXX 14-I
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N-PSDB; AAA11281.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grotendorst GR,
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14-DEC-1998;
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(FIBR-) FIBROGEN INC.
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98US-0112241P.
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This sequence represents a fragment of the human connective tissue growth factor (CTGF) polypeptide which has mitogenic activity. The sequence covers the amino acids encoded by exons 4 and 5 of the full length cDNA sequence (AAAN1280). The protein can be used to raise antibodies which specifically bind to CTFG and are used to treat a CTGF-associated disease or disorder, e.g. a fibroproliferative disease/disorder such as kidney fibrosis, scleroderma, pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and

New fragment of connective tissue growth factor (CTGF) polypeptide having mitogenic activity, useful in wound healing, bone and tissue repair.

Disclosure; Fig 3; 71pp; English.

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Best Local
                        Connective tissue growth factor (CTGF) (AAW12694) is a cysteine-rich mitogenic protein which is selectively induced in fibroblasts after activation with transforming growth factor beta (TGF-beta). Recombinant CTGF can be produced in prokaryotic or eukaryotic host cells utilising an isolated CTGF gene (AAT59618). Compsns. comprising CTGF, pref. in combination with TGF-beta, are used to induce bonding formation, e.g. to treat osteoporosis, osteoarchritis and osteochondrytis, to induce tissue and cartilage formation, and to induce wound healing. It can also be used in culture systems e.g. to expand stem cells or chondrocytes prior to reimplantation. CTGF is more stable to protease degradation than other growth factors used as prior art wound healing agents. (Updated on 25-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             retinopathy, hypertension, kidney disorders, angiogenesis-related disorders, skin fibrotic disorders, and cardiovascular disorders. protein is also useful in wound healing, bone and tissue repair
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             growth factors used -2003 to correct PR
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                                                                                                                                                                                                                                      Connective Tissue Growth Factor composition - and cartilage formation and wound healing.
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31-MAY-1996;
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31-MAY-1997
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osteoporosis; osteoarthritis; osteochondrytis.
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96WO-US008140.
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               as prior art field.)
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Pred. No. 1.7e-85;
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                                 The present invention describes human small CCN-like growth factor (SCGF). SCGF has vulnerary and osteopathic activities, and can be used i gene therapy. The SCGF polypeptides and polynuclectides can be used for treating muscle wasting diseases, and osteoporosis, and to stimulate wound healing and tissue regeneration, to promote angiogenesis and to stimulate proliferation of vascular smooth muscle and endothelial cell production. The present sequence represents a CNN family protein which i given in comparison with the human SCGF in the exemplification of the
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01-APR-1998;
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                                                                                                                                                                Disclosure;
                                                                                                                                                                                                       Novel isolated polynucleotide sequence encoding a human small CCN-like growth factor, useful for treating muscle wasting disease, and
                                                                                                                                                                                                                                              WPI; 2002-382150/41.
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                                                                                                                                                                                          osteoporosis.
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98US-00053587.
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Pred. No. 3.9e-85;
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wound healing;
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Best Local Similarity Matches 172; Conserv

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<u>,</u>

Mismatches

. 3.9e-85; ches 0; DB 5;

Indels

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Gaps

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Length 348;

Score 956; Pred. No. 3

Query Match Best Local

Sequence

348 AA;

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Query Match
Best Local S
Matches 172
                                                                                                                                                               Novel human connective tissue growth factor (CTGF) (AAR79964) is related immunologically and biologically to platelet-derived growth factor (PDGF), but is the product of a distinct gene. CTGF is mitogenic and also a chemotactic agent for cells. It is produced by endothelial and fibroblastic cells, and probably acts as a growth factor in wound healing. Recombinant CTGF can be obtd. by expression of cDNA clone bB60R32 (AAT04226) in transformed host cells. It is used to accelerate wound healing, and to raise antibodies useful in detecting disorders associated with overgrowth of cells, such as cancer, fibrotic diseases and atherosclerosis. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Connective tissue growth factor; CTGF; wound healing; vulnerary; cell proliferation; cancer; fibrosis; atherosclerosis; diagnosis therapy;
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12-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New connective tissue growth factor - used to develop prods. for wound healing and for diagnosis and therapy of cell proliferative disorders.
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     Local Similarity
les 172; Conserv
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DB; AAT04226.
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     Score 956; DB 2;
Pred. No. 3.9e-85;
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                          This sequence represents the human connective tissue growth factor (CTGF). CTGF is related immunologically and biologically to platelet-CC (CTGF). CTGF is related immunologically and biologically to platelet-GC derived growth factor (PDGF), but is encoded by an unrelated gene. CTGF is thought to play a significant role in the normal development, growth, CC and repair of human tissue, similarly to PDGF. The cDNA encoding this CC sequence was isolated by screening a cDNA library from human umbilical CC vein endothelial (HUVE) cells with anti-PDGF antibodies. CTGF can be used CC diagnostic of proliferative diseases involving outgrowth of connective CC diagnostic of proliferative diseases involving outgrowth of connective CC of these diseases can be treated with reagents reactive with CTGF, such CC acids, and ribozymes could also serve as assay reagents). Antisense nucleic advantage with using CTGF is that it is more stable, and less susceptible CC droptease degradation than PDGF, and other growth factors involved in CC (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
18-MAR-1997
                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding connective tissue growth accelerating wound healing, also for diagnosis and proliferative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Connective tissue growth factor; CTGF; human; connective tissue cel proliferative disease; platelet-derived growth factor; PDGF; develo tissue growth; repair; umbilical vein endothelial cell; HUVE cell; antibody; wound healing; cancer; fibrotic disease; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Connective tissue growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grotendorst GR,
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14-DEC-1993;
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                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                 9; Col 15-18; 11pp; English
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93US-00167628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     development;
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Best Local
Novel human connective tissue growth factor (CTGF) (AAW09089) is a PDGF-immunorelated protein that may play a significant role in the normal development, growth and repair of human tissue and probably functions as a growth factor in wound healing. CTGF may be involved in diseases in which there is an overgrowth of connective tissue cells, such as cancer, tumour formation and growth, fibrotic diseases (e.g. pulmonary fibrosis, kidney fibrosis, glaucoma) and atherosclerosis. Recombinant CTGF can be produced in transformed host cells utilising a cDNA clone isolated from a HUVEC library. It can be used to accelerate wound healing. CTGF
                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                             Connective
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31-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human connective tissue growth factor.
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26-APR-1997
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                                                                                                                                                                                                                                                                                                                       treatment
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DB; AAT45360, AA
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                                                                                A method has been developed for ameliorating a cell proliferative disorder associated with connective tissue growth factor (CTGF). The method comprises the administration of an antibody or its fragment that binds to CTGF and not to platelet-derived growth factor (PDGF), to the site of the disorder. CTGF is related immunologically and biologically to PDGF. The present sequence represents CTGF. The method is used to treat conditions involving the overgrowth of connective tissue cells such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 platelet derived atherosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                  Ameliorating cell proliferative disorder associated with connective tissue growth factor - comprises the administration of an antibody wibinds to connective tissue growth factor and not to platelet-derived
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10-FEB-1995;
02-JUN-1995;
This represents the amino acid sequence of connective tissue growth factor (CTGF). This can be used in the method of the invention for inducing bone or tissue formation that comprises administration to a patient, a composition comprising CTGF and a carrier. CTGF can also be used in a method for inducing wound healing. The methods can be used for inducing wound healing. The methods can be used for inducing bone, tissue or cartilage formation in disorders such as osteoporosis, osteoarthritis or osteochondrytis, arthritis, skeletal disorders, hypertrophic scars, burns, vascular hypertrophy, or in wound healing. The CTGF and functional fragments are more stable and less
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                SOUTH FLORIDA.
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93US-00167628.
95US-00386680.
95US-00459717.
                                                                                                                                                                                                                                                                                                                                                                         9608-00656393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "signal peptide" 22. .349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth factor (CTGF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "mature protein"
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Pred. No. 3.9e-85;
; Mismatches 0;
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                                                                                                                                                                       factor -
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                                                                                                                                                           inducing
                                                                                                                                                            for inducing bone, tis
inducing wound healing.
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ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC

Similarity

Conservative

0

Indels

0

Gaps

0

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RESULT 9
AAY18361
ID AAY1
XX AAY1
AC AAY1
XX CTGG
KW CTGGI
KW CTGGI
KW CTGI
XX USS:
XX I14-
PFF 20-1
XX UFFF 20-1
XX UFFF
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Query Match
Best Local S
Matches 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-1993;
10-FEB-1995;
11-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            susceptible to protease degradation than platelet derived growth factor (PDGF) and other growth factors known to be involved in wound healing
                                                                                                                                         This sequence is the human connective tissue growth factor (CTGF). The invention relates to a method of detecting a cell proliferative disorder comprising comparing the level of CTGF in a sample against a control, where an increase is indicative of a cell proliferative disorder (fibrotic disease or atherosclerosis). The method is used to detect cell proliferative disorders such as fibrotic disease and atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                    Detecting cell patherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGF; connective tissue growth cell proliferative disorder; at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY18361
                                                                                              Sequence 349
                                                                                                                                                                                                                                                                                                                 Disclosure; Col 15-18; 11pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-384720/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVINDNASCRLEKQSRLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; illarity 100.0%; Conservative
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95US-00386680.
96US-00712302.
                                                                                                                                                                                                                                                                                                                                                                                           proliferative disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00880031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   th factor; human; atherosclerosis;
Score 956; D
Pred. No. 3.9
O; Mismatches
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Pred. No. 3.9e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor.
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                         956; DB 2;
No. 3.9e-85;
                                                                                                                                                                                                                                                                                                                                                                                                  as fibrotic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fibrotic disease; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
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RESULT 10
AAY92939
ID AAY92939
ID AAY92939
ID AAY92939
XX AAY92
XX OB-NO
DE Human
XX Derma
KW nephri
KW vulne
KW crofe;
KW myofi;
KW fibrc
XX Homo
XX Clain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
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                                                                                                                                                                                polypeptide having the ability to induce extracellular matrix synthesis, collagen synthesis and/or myofibroblast differentiation. The invention relates to fragments of CTGF, especially those encoded by exons 2 and/or 3, which contain the inductive activity. The protein and/or fragments can be used to raise antibodies and the coding sequence can be used to generate antisense oligonucleotides. The antibody or antisense sequence against the CTGF sequence can be used in a method to treat a CTGF-associated disease or disorder such as a fibroproliferative disease or disorder, especially selected from kidney fibrosis, scleroderma, pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and retinopathy, hypertronsion, kidney disorders, angiogenesis-related disorders, skin fibrosic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dermatological; antiarthritic; antiarteriosclerotic; antidiabetic; nephrotropic; ophthalmological; hypotensive; cardiant; tranquilizer; vulnerary; antiinflammatory; human; connective tissue growth factor; CTGF; extracellular matrix synthesis; collagen synthesis; antibody; myofibroblast differentiation; antisense; fibroproliferative disease;
                                                                                   disorders, and cardiovascular disorders. The disease or disorder can also be selected from acute or repetitive traumas (including surgery or radiation therapy, and fibrosis of organs), diseases caused by vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fragment of connective tissue growth factor, useful for treating fibroproliferative diseases or disorders, including kidney fibrosis, scleroderma, arthritis, hypertropic scarring, atherosclerosis, diabe nephropathy and retinopathy.
                                                                endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a human connective tissue growth factor (CTGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grotendorst GR;
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14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tibrosis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human connective tissue growth factor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY92939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Fig 3A-B; 74pp; English.
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   cell proliferation or migration (including cancers), bowel disease, Crohn's disease, joint inflammation, disease, dermatological diseases, diabetes, and kel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                          This sequence represents a human connective tissue growth factor (CTGF) polypeptide which has mitogenic activity. The protein can be used to raise antibodies which specifically bind to CTFG and are used to treat (CTGF-associated disease or disorder, e.g. a fibroproliferative disease/disorder such as kidney fibrosis, scleroderma, pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring, atherosclerosis, diabetic nephropathy and retinopathy, hypertension, kidney disorders, anglogenesis-related disorders, skin fibrotic disorders, and cardiovascular disorders. The protein is also useful in disorders, and cardiovascular disorders. The protein is also useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-2000
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14-DEC-1998;
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  Sequence
                                                   wound healing, bone and
                                                                                                                                                                                                                                                                                                                                                                Claim 2,
                                                                                                                                                                                                                                                                                                                                                                                                                      mitogenic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                      New fragment of connective tissue growth factor (CTGF) polypeptide having mitogenic activity, useful in wound healing, bone and tissue repair.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FIBR-) FIBROGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        connective tissue growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  connective tissue growth factor;
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     349
                                                                                                                                                                                                                                                                                                                                                                Fig 2A-B; 71pp; English.
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98US-0112241P.
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                                                            tissue repair
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Pred. No. 3.9e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor protein.
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Query Match
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Matches 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Connective tissue growth factor; CCN growth factor; Degree transfer to basic fibroblast growth factor; DFGF; neovascular; andthelial cell proliferation; retinal; haemangioma; leukaemia; metastasis; psoriasis; tumour; glaucoma; diabetic retinopathy; arthritis; endometriosis; Insulin-like growth factor-binding domain; IGF; von Willabrand factor type C repeat; Thrombospondin type 1 domain; von willabrand factor type C repeat; Thrombospondin type 1
                                                                                                                                                                                                             The present sequence is human connective tissue growth factor, which is a member of CCN growth regulator family. It has antiangiogenic activity and is a potent inhibitor of basic fibroblast growth factor (bFGF) -timulated bovine endothelial cell proliferation. It contains Insulin-like growth factor (IGF)-binding domain, von Willebrand factor type C repeat, Thrombospondin type 1 domain and C-terminal cysteine knot profile (CTCK)-2 domain. It can be used to treat conditions associated with abnormal angiogenesis or neovascularisation like, retinal neovascularisation, tumour growth, haemangioma, solid tumours, leukaemia, metastasis, psoriasis, neovascular glaucoms, diabetic retinopathy, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New anti-angiogenic protein containing an IGF binding, Willebrand type C, thrombospondin type I and cysteine knot domains is useful inhibiting atopic angiogenesis e.g. in solid tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human connective tissue growth factor
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                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 26-27; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-182688/16
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                                                                                                                                                                                       endometriosis and premature retinopathy
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                               100.0%; Score 956; DB 3; 100.0%; Pred. No. 3.9e-85;
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The specification describes a pharmaceutical composition, comprising a growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent inhibits the action of at least one specific adverse protein, i.e. a crowdease, that is upregulated in a damaged tissue such as a wound environment. Growth factors which are included in the composition of the cinvention are platelet-derived growth factor (PDGF), fibroblast growth factor (FGF), connective tissue derived growth factor (CTGF), continctive tissue derived growth factor 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transforming growth factor-beta; TGF-beta; matrix metalloproteinase; granulocyte macrophage colony stimulating factor; GM-CSF; uPA; vascular endothelial growth factor; urokinase plasminogen activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth factor; protein inhibitor; protease; damaged tissue; platelet-derived growth factor; PDGF; fibroblast growth factor; FGF; connective tissue derived growth factor; CTGF; chrysalin; VEGF; keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
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                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences on number of human shear stress response proteins. These are useful diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis a
                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequences, proteins encoded by them and antibodies against useful in diagnosis and treatment of vascular disease caused by arteriosclerosis.
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N-PSDB; AAH02914.
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Pred. No. 3.9e-85;
; Mismatches 0;
                                                                                            Score 956; DB 4;
Pred. No. 3.9e-85;
; Mismatches 0;
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Sugano S;
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Query Match
Best Local S
Matches 172
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14-DEC-1993;
10-FEB-1995;
11-SEP-1996;
                                                                           The invention relates to a method for the recombinant production of human connective tissue growth factor (CTGF; AAB60664), involving transforming a prokaryotic or enkaryotic host cell with an expression construct comprising the CTGF cDNA sequence (AAF59954) or a fragment thereof, and culturing the host cell under conditions suitable for the expression of CTGF. CTGF is a mitogen and chemotactic agent for connective tissue cells and plays a significant role in normal development, growth and repair of human tissues. It is useful as a therapeutic for accelerating wound healing and promoting normal healing mechanisms and may therefore be used in the treatment of e.g., burns. CTGF is also useful as a diagnostic reagent for diagnosing pathological states in a patient suspected of having a disease characterised by a disorder of cellular proliferation. The present sequence represents human CTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitogenic; chemotactic; tissue u wound healing; vulnerary; diagno cellular proliferation disorder.
                                                                                                                                                                                                                                                                                                 producing connective tissue growth factor involves transforming cell with polynucleotide encoding the growth factor and growing under optimum conditions so that the polynucleotide is expressed
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                                                      Sequence
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               Local Similarity
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DB; AAF59954.
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93US-00167628.
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Pred. No. 3.9e-85;
; Mismatches 0;
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Qy 61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKPGGVCTDGRCCTPHR 120

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Title:
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PIR 80:*
1: pir1:*
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3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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956
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                                                                                                                                                                                                                                                                                   283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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otogelin - mouse	secreted Leucine-r	hionein-2	hypothetical prote	protein C37C3.6a [thrombospondin pre	circumsporozoite p	probable tenascin	hypothetical prote	lone	hypothetical prote			procollagen N-endo	hypothetical prote			F-spondin precurso	immunodominant mic	F-spondin - rat	protein CTRP - mal	angiogenesis inhib			gene CYR61 protein	gene novH protein	NOV protein - chic	beta IG-M2 protein		Description	

RESULT 2
A40578
beta IG-M2 protein precursor - mouse
beta IG-M2 protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Aate: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 31-Dec-2004
C;Aate: 06-0578; A53228
C;Accession: A40578; A53228
R;Brunner, A.; Chim, J.; Neubauer, M.; Purchio, A.F.
DNA Cell Biol. 10, 293-300, 1991
DNA Cell Biol. 10, 293-300, 1991
A;Title: Identification of a gene family regulated by transforming growth factor-beta.
A;Reference number: A40578; MUID:91229699; PMID:2029337

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ALIGNMENTS

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	용 성
Query Match 100.0%; Score 956; DB 2; Length 349; Best Local Similarity 100.0%; Pred. No. 1e-76; Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Ma B Q
A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-349 <oem> A;Cross-references: UNIPARC:UPI000003FD13; EMBL:X78947; NID:g474933; PID:g474934 C;Superfamily: IGFBP-related protein, CNN type</oem>	A; St A; Mo A; Re A; Cr C; Su
submitted to the EMBL Data Library, April 1994 A;Description: Differential cloning and expression of human connective tissue growth far A;Reference number: S44205 A;Accession: S44205	subm A;De A;Re A;Ac
A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-349 <bra> A;Cross-references: UNIPROT:P29279; UNIPARC:UPI000003FD13; GB:M92934; GB:M36965; GB:S56. R;Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.</bra>	A;Re A;Cr
C;ACCEBBION: A4031; 344203 R;BERADHAM, D.M.; Iggarabhi, A.; Potter, R.L.; Grotendorst, G.R. J. Cell Biol. 114, 1285-1294, 1991 A;Pitle: Connective tissue growth factor: a cysteine-rich mitogen secreted by human vasc A;Reference number: A40551; MUID:91373462; PMID:1654338	R; Bra R; Bra A; Til
A40551 A40551 connective tissue growth factor - human C;Species: Homo sapiens (man) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-2004	A40551 connec C;Spec C;Date

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RESULT .
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A;Title: Structure, mapping, and expression of fisp-12, a growth factor-inducible gA;Reference number: A53228; MUID:91363290; PMID:1888698
A;Accession: A53228
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C;Superf
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C;Superfami
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Gallus gallus (chicken)
C;Species: 19-Reb-1994 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C;Date: 19-Reb-1994 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C;Date: 19-Reb-1992 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C;Date: 19-Reb-1992 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
Roll Cell Biol 12, 10-21, 1992 #sequence_revision 0 for the control of the control o
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A;Residues: 1-160,'K',162-348 <RYS>
A;Cross-references: UNIPARC:UPI000003FD12; GB:M70641; NID:g193313; PIDN:AAA37627.1;
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A; Residues: 1-351 <JOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALAAYRLEDTFGPDFTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNTFCRLEXQSRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTLPVEFKCPDGEVMKKNWMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
                                                                                                                                                                                                                                                                                                           MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
                                                                                                                                                                                                                                                                                                                                                                            AMAAYRQEATLGIDVSDSSANCIEQTTEWSACSKSCGMGFSTRVTNRNQQCEMVKQTRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                      ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
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                                                                                                                                                                                       TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF 159
                                                                                                                                                                                                                                                     MMRPCENE-EPSDKKGKKCIQTKKSMKAVRFEYKNCTSVQTYKPRYCGLCNDGRCCTPHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGFBP-related protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.2%; Sco
59.7%; Pre
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95.9%;
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Pred. No. 8.8e-75;
Pred. matches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 546.5;
Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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gene CYR61 protein precursor - mouse (Species: Mus musculus (house mouse) (;Species: Mus musculus (house mouse) (C;Date: 28-Sep-1990 #sequence revision 18-Nov-1992 #text_change 31-Dec-2004 C;Accession: A35669; 148319; $16446 R;O'Brien, T.P.; Yang, G.P.; Sanders, L.; Lau, L.F. Mol. Cell. Biol. 10, 3569-3577, 1990 A;Title: Expression of cyr61, a growth factor-inducible immediate-early gene A;Reference number: A35669; MUID:90287146; PMID:2355916 A;Accession: A35669; MUID:90287146; PMID:2355916
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A.;Title: Structural analysis of the human nov proto-oncogene and A.;Reference number: 138069; MUID:94336229; PMID:7520150
A;Accession: 138069
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                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P18406; UNIPARC:UPI0000022DFF; GB:M32490; NID:g192909; PIDN: A;Note: the authors translated the codon GAT for residue 337 as Gln R;Latinkic, B.V.; O'Brien, T.P.; Lau, L.F. Nucleic Acids Res. 19, 3261-3267, 1991
Nucleic Acids Res. 19, 3261-3267, 1991
A;Title: Promoter function and structure of the growth factor-inducible immediate early A;Reference number: 148319; MUID:91288203; PMID:2062642
A;Accession: 148319
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                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-379 <RES>
A;Cross-references: UNIPARC:UPI0000022DFF; EMBL:X56790; NID:g50632; PIDN:CAA40109.1;
A;Note: the authors did not translate the codon for residue 108
A;Note: the authors translated the codon GAT for residue 337 as Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 28/3; 104/1; 188/1; 259/3
C;Superfamily: IGFBP-related protein, CNN type
F;203-250/Domain: thrombospondin type 1 repeat homology
                                                                                                         A;Introns: 21/3; 93/1; 208/1; 279/3
C;Superfamily: IGFBP-related protein, (
F;99-166/Domain: von Willebrand factor
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                                                                                                                                                                                          A;Gene: CYR61
                                                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-379 < OAB>
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;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 VRPCEQEPEQPTDKKGKKCLRTKKSLKAIHLQFKNCTSLHTYKPRFCGVCSDGRCCTPHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 VRPCEADLEE-NIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF-ESLYYRKMYGDM 171
51.0%; Score 487.5; DB 2; ilarity 49.4%; Pred. No. 1.7e-35; Conservative 32; Mismatches 44;
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Pred. No. 2.7e-38;
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or type C ;
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                                                             379;
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A;Reference number: Z19413

A;Recession: T21371

A;Stactus: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-2165 <WIL>
A;Residues: 1-2165 <WIL>
A;Cross-references: UNIPROT:Q19791; UNIPARC:UPI000007CF95; EMBL:Z69360; PIDN:CAA93287.1;
A;Experimental source: clone F25H8

R;Gajadsty, S.
submitted to the EMBL Data Library, February 1996

A;Reference number: Z19949

A;Accession: T24896

A;Reference number: Z19949

A;Accession: T24896

A;Residues: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-2165 <WI2>
A;Residues: 1-2165 <WI2>
A;Cross-references: UNIPARC:UPI000007CF95; EMBL:Z69361; PIDN:CAA93288.1; GSPDB:GN00022;
A;Genetics: Sep:F25H8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Simmons, D.L.; Levy, D.B.; Yannoni, Y.; Erikson, R.L. proc. Natl. Acad. Sci. U.S.A. 86, 1178-1182, 1989
A;Title: Identification of a phorbol ester-repressible v-src-inducible A;Reference number: A41428; MUID:89145206; PMID:2537491
A;Accession: A41428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEF-10 protein precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 03-Apr-1992 #sequence_revision C;Accession: A41428
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                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F25H8.3 - Caenorhabditis elegans
(;Species: Caenorhabditis elegans
(;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21371; T24896
R;Gajadaty, S.
R;Gajadaty, S.
R;Gajadaty, S.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19413
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A; Residues: 1-375 <SIM>
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Best Local S
Matches 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT: P19336; UNIPARC: UPI0000127478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCGQPYYSSLKKGKKCSKTKKSPEPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGSEPQSRAFENPKCI VQTTSWSQCSKTCGTGISTRVTNDNPDCKLIKETRICEVRPCGQ
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Pred. No. 8.3e-35;
7; Mismatches 49
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A; Cross-references: UNIPROT: Q8MYA8; UNIPARC: UPI0000075CEB;
A; Cross-references: Clone C02B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiogenesis inhibitor homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T18856; T24653
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A; Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, A,Reference number: Z19031 A,Accession: T18856
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                                                                                                                                                                                                 A;Gene: CESP:C02
A;Map position:
A;Introns: 25/3;
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A;Residues: 1-1444 <WI2>
A;Cross-references: UNIPARC:UPI0000075CEB;
                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T24653
                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data A; Reference number: Z19917
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                                                                                                                                                                                                                                                                  A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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Matches
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                                                                                                                                                                                                   25/3; 70/3;
                                 83
                                                                                              27 TEWSACSKTCGM-GISTR---VTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRT
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PRWSEWSSWSACSCFSLTSTRRRFCQVVDPTVQGFCAGAILEQIPCAPGSC 1182
                                 PKISKPIKFELSGCTSMKTYRAKFCGV---
                                                                SDWSSCSKSCGQDGIQTRQKLCLFNNAECSSYAESRRCKDLPSCSSISSGRTISENGFDA
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nilarity 21.3%;
Conservative 3:
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                                                                                                                                                                                                   96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2;
                                                                                                                                                  11.2%; Score 107; DB 2; 26.1%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                        Library,
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Pred. No. 0.037;
1; Mismatches
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                                                                                                                                      Mismatches
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                                                                                                                                                                   Length 1444;
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protein CTRP - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18397

RP - malaria parasite (Plasmodium falciparum) Plasmodium falciparum

R;Trottein,

Triglia,

T.; Cowman,

T18397 RESULT

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C;species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A38152
R;Klar, A.; Baldassare, M.; Jessell, T.M.
Cell 69, 95-110, 1992
A;Title: F-spondin: a gene expressed at high levels in the floor plate encod A;Reference number: A38152; MUID:92208952; PMID:1555244
A;Accession: A38152
A;Cession: A38152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-807 <KLA>
A; Residues: 1-807 <KLA>
A; Residues: 1-807 <KLA>
A; Cross-references: UNIPROT: P35446; UNIPARC: UPI000012AC71; GB: M88469; NID: g204176; PIDN: A; Cross-references: UNIPROT: P35446; UNIPARC: UPI000012AC71; GB: M88469; NID: g204176; PIDN: A; Cross-references: UNIPROT: P1840
A; Note: sequence extracted from NCBI backbone (NCBIN: 90877, NCBIP: 90878)
C; Superfamily: F-spondin; thrombospondin type 1 repeat homology <THR2>
F; 540-555; Domain: thrombospondin type 1 repeat homology <THR4>
F; 557-611 / Domain: thrombospondin type 1 repeat homology <THR1>
F; 667-721 / Domain: thrombospondin type 1 repeat homology <THR1>
F; 667-721 / Domain: thrombospondin type 1 repeat homology <THR6>
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A38152
F-spondin -
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A,Molecule type: DNA
A,Residues: 1-2098 <TRO>
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A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a
A;Reference number: Z18926; MUID:96360471; PMID:8719155
A;Accession: T18397
immunodominant microneme protein Etp100 - Eimeria tenella
C;Species: Eimeria tenella
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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                                                                            A45638
                                                                                                RESULT 11
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                               ANCLY-QTTEWSACSKTCGMGISTR-----VTNDNASCRLE-KQSRLCMVRPCE----
                                                                                                                                                                                                                                                                    LSPWSEWSDCSVTCGKGMRTRQRMLKSLAELGDCNEDLEQAEKCM-LPEC--PIDCELSE
                                                                                                                                                                                                                                                                                                                                                                       SSCLVTEWGEWDDCSATCGMGMKKRHRMVKMSPADGSMCKAETSQAEKCMMPECHTIPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CTPHRTTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDND
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                                                                                                                                                                                                                       CTSMKTYRAKFCGVCTDGRCCTPH--RTTTLPVE----FKCPDGEVMKK 138
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23.8%; Pred. No. 0.55;
tive 21; Mismatches
                                                                                                                                                                        ---KGHMIRTRTIQMEPQFGGAPCPETVQRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101.5; DI
Pred. No. 0.28;
9; Mismatches
                                                                                                                                                                                                                                                                                                                      ----ADLEENIKKGKKCIRTPKISKPIKFELSG
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RESULT 12
A47723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-712 <TOM>
A;Residues: 1-712 <TOM>
A;Ross-references: UNIPROT:043981; UNIPARC:UPI000007B8B2; GB:AF032905; GB:M73495;
A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756)
A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756)
F;48-218/Domain: von Willebrand factor type A repeat homology <VWA1>
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R;TomLey, F.M.; Clarke, L.B.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Biochem. Parasitol. 49, 277-288, 1991
Mol. Biochem. Parasitol the gene encoding an immunodominant microneme protein of Eimeria ter A;Title: Sequence of the gene encoding an immunodominant microneme protein of Eimeria ter A;Reference number: A45638; MUID:92131064; PMID:1775171
                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-803 <RUZ:
A;Cross-references: UNIPROT:P35447; UNIPARC:UPI000012AC72; GB:L09123; NID:g409244; PIDN:
A;CySuperfamily: F-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A. Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A;Title: Ectopic neural expression of a floor plate marker A;Reference number: A47723; MUID:93376785; PMID:8367492
A;Accession: A47723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F-spondin precursor - African clawed frog C;Species: Xenopus laevis (African clawed C;Date: 27-Jun-1994 #sequence_revision 27-C;Accession: A47723
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FKCPDGEVMKKNMMFIKTCACH 149
                                                                                                                                                                                                   LVQTTEWSACSKTCGMG--ISTRVTN-----DNASCRLEKQSRLCMVRPCE----ADLEEN
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                                                   LKDAREKRRSEKIKEDSDGEQYPVCKMKPWTAWTECTKFCGGGIQERFMTVKKRFKSSQF
                                                                                                 IKKGKKCIRTPKISKPIKFELSGCTSMKTYRA----KFCGVCTDGRCCTPHRTTTLPVE 127
                                                                                                                                                     LTEWSYWSECNKSCGKGHMIRTRMITMEPQFGGAVCPETVQRKKCRLRKCQKSSGNERRH
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Pred. No. 0.41;
9; Mismatches
                                                                                                                                                                                                                                                                           Score 99; DB 2
Pred. No. 0.46;
                                                                                                                                                                                                                                                      Mismatches
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27-Jun-1994
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F;1054-1095/Domain: LDL receptor ligand-binding repeat hom F;1101-1138/Domain: LDL receptor ligand-binding repeat hom F;1146-1182/Domain: LDL receptor ligand-binding repeat hom F;1187-1233/Domain: LDL receptor ligand-binding repeat hom F;128-1263/Domain: LDL receptor ligand-binding repeat hom F;1270-1307/Domain: LDL receptor ligand-binding repeat hom F;1370-1307/Domain: LDL receptor ligand-binding repeat hom F;13159-1396/Domain: LDL receptor ligand-binding repeat hom F;13159-1396/Domain: LDL receptor ligand-binding repeat hom F;13159-1396/Domain: LDL receptor ligand-binding repeat hom F;1341-1475/Domain: LDL receptor ligand-binding repeat hom F;1311-1654/Domain: LDL receptor ligand-binding repeat hom F;2012-2029/Domain: LDL receptor ligand-binding repeat hom F;2014-1475/Domain: LDL receptor ligand-binding repeat hom F;2014-1475/Domain: LDL receptor ligand-binding repeat hom F;2014-2012/Domain: LDL receptor ligand-binding repeat hom F;2014-1475/Domain: LDL receptor ligan
    F;3586-3623/Domain:
F;3627-3666/Domain:
F;3671-3705/Domain:
F;3709-3746/Domain:
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F;53-87/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;93-131/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;138-175/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;138-218/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;182-218/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;223-257/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;230-257/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;262-297/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;302-336/Jomain: EGF homology <EGF1>
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A;Residues: 1-4753 <YOC>
A;Residues: 1-4753 <YOC>
A;Cross-references: UNIPROT:Q04833; UNIPARC:UPI000013C4B5; GB:M96150; NID:g156359;
A;Note: nucleotide sequence not given; translation not complete in this paper
R;Yochem, J.; Greenwald, I
submitted to the EMBL Data Library, July 1992
A;Description: A gene for an LDL receptor-related protein (LPR) in the nematode C.e
A;Reference number: S27801
A;Accession: S27801
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A;Title: A gene for a low density lipoprotein receptor-related protein A;Reference number: A47437; MUID:93281621; PMID:8506301
A;Accession: A47437
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submitted to the EMBL Data
A;Reference number: Z19439
A;Accession: T21547
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F;3006-3044/Domain:
F;3049-3093/Domain:
F;3100-3135/Domain:
F;3140-3174/Domain:
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;Residues: 1-4753 <YO2>
;Cross-references: UNIPARC:UPI000013C4B5; EMBL:M96150; NID:g156359; PIDN:AAA28105.1;
                                                                                                                                                                                                                                                                                                                                                                                                                               ,2874-2912/Domain:
,2919-2956/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Introns: 31/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: LPR
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F;3753-3788/Domain: I
F;3793-3830/Domain: I
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F;3917-3951/Domain: I
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T29247
hypothetical protein DKFZp434H204.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 30-Sep-1999 #sequence 0.;Datesion: T14764
C;Accession: T14764
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-654 <MIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid A;Reference number: Z20594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F09F9.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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F;4092-4130/Domain:
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F;4000-4040/Domain:
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                                                                                                                                                                                                                                                                                                                                                                84 KISKPIKFELS---GCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPV--EFKCPDGEVMKK 138
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29.2%;
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Pred. No.
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Pred. No. 0.
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated

- permanent accession numbers. The new UniProt record may not contain the previous temporary accession number. numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession
- accession number can be found by searching the old accession number in the UniProt Protein extension .rup) that can no longer be found in the database, the permanent record with the new If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher

numbers members of the public who may encounter UniProt temporary accession include a copy of this attachment to assist any future Examiners or When submitting sequence search results for scanning into IFW, please

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Oemar B.S., Werner A., Garnier J.M., Do D.D., Godoy
Marz W., Rupp J., Pech M., Luescher T.F.;
"Human connective tissue growth factor is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91373462; PubMed=1654338; DOI=10.1083/jcb.114.6.1285; Bradham D.M., Igarashi A., Potter R., Grotendorst G.R.; Bradham D.M. Igarashi A., Potter R. B., Grotendorst G.R.; "Connective tissue growth factor: a cysteine-rich mitogen secreted human vascular endothelial cells is related to the SRC-induced human vascular endothelial cells is related to the SRC-induced immediate early gene product CEP-10.";
                                                                                                                                                                                                   Li Q.-H., Wang L.-C., Liu L.-D., Dong S.-Z Wang J., He S.-Q., Dong C.-H., Zhao S.-D., "Expression, purification and bio-activity
                                                                                                                                                                                                                                                                                                                                            atherosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93187114; PubMed=1293144; Igarashi A., Bradham D.M., Okochi H., "Connective tissue growth factor.";
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Homo sapiens (Human).
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95:831-839(1997).
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114:1285-1294(1991).
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RA Milning L. Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA Milning L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA Almeida J.G.R., Clamp M.E., Bethel G., Milne S., Alinscough R.,
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.
RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
RA Barlow K.F., Bares K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Barlow Y.S., Bary-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA Blakey S.E., Barrill W., Burton J., Carder C., Carter N.P.,
RA Blakey S.E., Barrill W., Burton J., Carder C., Carter N.P.,
RA Collier R.E., Collinn S.B., Colman L.K., Corby N.R., Coville G.J.,
RA Collier R.E., Collinn J.E., Colman M., Fanthrowl M.E.,
RA Collier R.E., Toollinn J.E., Colman M., Fanthrowl M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Gribble S., French L., Garner P., Garnett J., Ghori M.J.,
RA Gribble S., French L., Garner P., Garnett J., Ghori M.J.,
RA Gribble S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,
RA Gribble S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,
RA Humphray S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Howden P.J., Howe K.L., Howell G.R., Lloyd D.M.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Kay M., Keenan S.J., McCann O.T., McLaren S.J., McLay K.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammdi M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammdi M.,
RA Loveland J.E., Succe C.D., Smith S., Smith M., Spraggon L.,
RA Malla M., Walley J., McLay K., Spraggon L.,
RA Marlier A., Fater A., Patel R.,
RA Marlier A., Steward C.A., Sycamore N., Tandyn-Hall G., Tester J.,
RA Marlier A., Walley D.J., Milley D.J., Wilner T.E., Mood J.M., Wray P.W.,
RA Myatt J.C., Young L., Vounger R., Milley D.J., Wilner T.E., Mood J.M., Wra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rnelan M., Farmer A.;
"Cloning of human full-length CDSs in vector.";
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Koundinya M., Raphael J., Moreira D.,
Phelan M., Farmer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakanishi T., Nishida T., Shimo T., Kob
Tamatani T., Tezuka K., Takigawa M.;
"Effects of CTGF/Hcs24, a product of a
specific gene, on the proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mungall
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                                                      HEPARIN-BINDING, AND CELL ADHESION.

MEDLINE=22442376; PubMed=12553878; DOI=10.1677/joe.0.176R001;

Ball D.K., Rachfal A.W., Kemper S.A., Brigstock D.R.;

"The heparin-binding 10 kDa fragment of connective tissue grofactor (CTGF) containing module 4 alone stimulates cell adhes

J. Endocrinol. 176:R1-R7(2003).
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                                                                                                                                                                                              Endocrinology 141:264-273 (2000).
                                                                                                                                                                                                                   chondrocytes in culture.
                                                                                                                                                                                                                                                                                                                  TISSUE=Chondrocyte;
MEDLINE=20080284; P
                                                                                                                                                                                                                                                                                                                                                                                               Nature 425:805-811(2003).
FUNCTION: Major connective tissue mitoattractant so vascular endothelial cells. Promotes proliferation differentiation of chondrocytes. Mediates heparin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  А.J.,
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                                                                                                                                                                                                                                                                                                PubMed=10614647; DOI=10.1210/en.141.1.264; nida T., Shimo T., Kobayashi K., Kubo T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=14574404;
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, Schatten R., Shen B., Henze
, LaBer J.;
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Scott C.E.,
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R MIM; 121009; ...

R GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.

R GO; GO:0005586; C:plasma membrane; TAS.

R GO; GO:0005520; F:insulin-like growth factor binding; TAS.

R GO; GO:0005520; F:insulin-like growth factor binding; TAS.

R GO; GO:0005514; P:response to wounding; TAS.

R GO; GO:0009511; P:response to wounding; TAS.

R InterPro; IPR006208; Cys_knot.

R InterPro; IPR006207; Cys_knot.

R InterPro; IPR012395; IGFBP_CNN.

R InterPro; IPR012395; IGFBP_LIKE.

R InterPro; IPR012096; IGFBP_LIKE.

R InterPro; IPR010084; TSP1.

DR Pfam; PF00007; Cys_knot; 1.

Pfam; PF00009; TSP_1; 1.

DR Pfam; PF00093; VWC; 1.

DR Pfam; PF00093; VWC; 1.

DR SMART; SM000121; IB; 1.

DR SMART; SM00121; IB; 1.

DR SMART; SM000121; IB; 1.

DR SMART; SM000121; TSP1; 1.

DR SMART; SM000209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M92934; AAA91279.1; -; mRNA.
EMBL; X78947; CAA55544.1; -; mRNA.
EMBL; AX95801; AAQ95223.1; -; mRNA.
EMBL; AX556024; AAS55639.1; -; mRNA.
EMBL; BT019794; AAV38597.1; -; mRNA.
EMBL; BT019795; AAV38597.1; -; mRNA.
EMBL; BT019795; AAV38598.1; -; mRNA.
EMBL; BT019795; CAG46559.1; -; mRNA.
EMBL; AL354866; CAC44023.1; -; Genomic_DNA.
EMBL; AL354866; CAC44023.1; -; Genomic_DNA.
EMBL; AL354866; CAC44023.1; -; Genomic_DNA.
                                                                                                                             PROSITE; PS01165; CTCK 1; 1.

PROSITE; PS01225; CTCK 2; 1.

PROSITE; PS01222; IGF BINDING; 1.

PROSITE; PS50092; TSPI; 1.

PROSITE; PS501206; VWFC 1; 1.

PROSITE; PS50184; VWFC 2; 1.

PROSITE; PS50184; VWFC 2; 1.

Alternative splicing; Cell adhesion; DN

Extracellular matrix; Glycoprotein; Her
                              Alternative splise Extracellular male SIGNAL 27 CHAIN 27 DOMAIN 33 DOMAIN 101 DOMAIN 198 DOMAIN 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collabout between the Swiss Institute of Bioinformatics and the EMBL outstate European Bioinformatics Institute. There are no restrictions can be along as its content is in no way modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÷
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SIMILARITY: Belongs to the CCN family.
SIMILARITY: Contains 1 CTCK (C-terminal cystine knot-like) domain.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 TSP type-1 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1; Synonyms=Long;
IsoId=P29279-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=2; Synonyms=Short;
IsoId=P29279-2; Sequence=VSP_002460;
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   101
101
198
247
286
   26
349
100
167
243
330
349
IGPBP.
VWFC.
TSP type-1.
CTCK.
Heparin-binding.
N-linked (GlcNAC.
                                                                                                   Connective
                                                                                                                 Potentia.
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Heparin-binding; Signal.
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Best Local Sim
Matches 172;
                                                                                           Query Match
Best Local Sim
Matches 172;
                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.

Halleck A., Ebert L., Mkoundinya M., Schick M., I

Meubert P., Kstrang K., Schatten R., Shen B., Her

Korn B., Zuo D., Hu Y., LaBaer J.;

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ dat

EMBL; CR541734; CA646534.1; -, mRNN.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005520; F:insulin-like growth factor binc

GO; GO:0001558; P:regulation of cell growth; IEA.

InterPro; IPR006207; Cys knot C.

InterPro; IPR00687; Inal gro_fac_pr.

InterPro; IPR00087; Inal gro_fac_pr.

InterPro; IPR000887; Inal gro_fac_pr.

R InterPro; IPR000887; Inal gro_fac_pr.

R InterPro; IPR001007; WWF C.

R InterPro; IPR001007; WWF C.

R Ffam; PF000219; IGFBP; 1.

R Ffam; PF000219; IGFBP; 1.

R Ffam; PF00093; VWC; 1.

R SMART; SM001041; CT; 1.

SMART; SM001041; TSP1; 1.

R SMART; SM001041; TSP1; 1.

R SMART; SM001214; WG; 1.
                                                                                                                                                                                            PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF BINDING; 1
PROSITE; PS50092; TSPI; 1.
PROSITE; PS011208; VWFC_1; 1.
PROSITE; PS011208; VWFC_2; 1.
SEQUENCE 349 AA; 38129 MW; 8
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Eukaryota; Metazoa; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
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                            1 ALAAYRLEDTFGPDDTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTLPVEFKCPDGBVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MVRPCEADLBENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
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Last sequence update)
Last annotation update)
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Pred. No. 5.6e-81;
); Mismatches 0;
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                                                                                                Score 956; DB 2;
Pred. No. 5.6e-81;
; Mismatches 0;
                                                                                                                                                                                                 8CC6999641511188 CRC64;
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                                                                                                                                                 Length 349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RC TISSUE-Peripheral Nervous System;

RM MEDLINE-22388557; PubMed=:12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschape C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

AN Altilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Habey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

AN Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

AN Hillian M., Madan A., Schmutz J., Myers R.M.,

ROdriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 172
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Homo sapie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Peripheral Nervous System;
Director MGC Project;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC087839; AAH87839.1; -; mRNA.
SEQUENCE 349 AA; 38069 MW; 0ECF8470B357EA95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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10-MAY-2005 (TYEMBLRel. 30, Last sequence update)
10-MAY-2005 (TYEMBLrel. 30, Last annotation update)
Connective tissue growth factor.
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Q5M8T4;
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                                               TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
                                                                                                                                 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
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                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                         Score 956; DB 2;
Pred. No. 5.6e-81;
Mismatches 0;
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RESULT

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O97765_PIG
D97765;
AC O97765;
AC O9766;
AC O1.MAY-1999
DT 01-MAY-1999
DC COLLECTIVE S
RN NUCLICOTIDE S
RN NUCLICOTIDE S
RC TISSUE=Uterr
OC NUCHI TAXID=9
RN NUCLEOTIDE S
RC TISSUE=Uterr
OC NUCHI TAXID=9
RN NUCLEOTIDE S
RC TISSUE=Uterr
OC NUCHI TAXID=9
RA HARTING POO.
DR GO; GO:00055
DR GO; GO:00055
DR GO; GO:00055
DR GO; GO:00055
DR InterPro; IE
DR INTERPOO.
DR SMART; SM000
DR Pfam; PPO0.
DR SMART; SM000
DR SM
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TGF BOVIN STANDARD; PRT; 349 AA.

C CTGF BOVIN STANDARD; PRT; 349 AA.

C 018739; OSCL71;
T 15-JUL-1998 (Rel. 36, Created)
T 28-FEB-2003 (Rel. 41, Last sequence update)
T 10-MAY-2005 (Rel. 47, Last annotation update)
E Connective tissue growth factor precursor.
N Name=CTGF; Synonyms=CCN2;
S Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harding P.A., Brigstock D.R.;

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ dat

REMBL; U70060; AAD00174.1; -; mRNA.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005520; F:insulin-like growth factor bine

GO; GO:0005520; F:insulin-like growth factor bine

REMBC; GO:0005520; F:insulin-like growth factor bine

GO; GO:0005520; F:insulin-like growth factor bine

REMBC; FRO001520; Cys knot; C.

RINterPro; IPR000627; Cys knot; C.

RINterPro; IPR000867; InsI_gro_fac_pr.

InterPro; IPR001007; VWF C.

RINterPro; IPR001007; VWF C.

RINTERPRO(11); ISP 1.

REMART; SM0011; ISP 1.

REMART; SM0011; ISP 1.

REMART; SM00121; INF; 1.

REMART; SM0121; INF; 1.

REMART; SM0121; INF; 1.

REMART; SM0121; INF; 1.

REM
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01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Eukaryota; Metazoa; Chordata; Crani:
Mammalia; Eutheria; Laurasiatheria;
Pecora; Bovidae; Bovinae; Bos.
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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97.7%;
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Pred. No. 9.1e-80;
4; Mismatches 0
                                    Craniata; Vertebrata; Euteleostomi; neria; Cetartiodactyla; Ruminantia;
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NCBI_TaxID=9913;

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RA Mathahs M., Schwitters C., Hove M., Rupp S., Erondu N.E.;
RT "Bovine connective tissue growth factor, organization of the
RT chromosomal gene and demonstration of promoter activity.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Major connective tissue micoattractant secreted by
CC vascular endothelial cells. Promotes proliferation and
differentiation of chondrocytes (By similarity). Mediates heparin-
CC and divalent cation-dependent cell adhesion in many cell types
CC including fibroblasts, myofibroblasts, endothelial and epithelial
CC cells (By similarity). Enhances fibroblast growth factor-induced
CC DNA synthesis (By similarity).
CC -- SUBUNIT: Monomer (By similarity).
CC -- SUBCELLULAR LOCATION: Found in the extracellular matrix and as a
CC soluble form (By similarity).
CC -- SIMILARITY: Contains 1 CTCK (C-terminal cystine knot-like) domain.
CC -- SIMILARITY: Contains 1 TSPB domain.
CC -- SIMILARITY: Contains 1 TSPB domain.
CC -- SIMILARITY: Contains 1 TYPC domain.
CC -- SIMILARITY: Contains 1 TYPC domain.
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InterPro; IPR006207; Cys_knot. C.
InterPro; IPR006207; IGFBP_CNN.
InterPro; IPR0012395; IGFBP_CNN.
InterPro; IPR000867; IGFBP_11ke.
InterPro; IPR000867; TSP1_INTERPRO; IPR001007; VWF_C.
InterPro; IPR001007; VWF_C.
INTERPRO; IPR001007; VWF_C.
INTERPRO; IPR001007; TSP1; 1.
INTERPRO; INT
                                                                                                                                                                                                                                                                                                                           PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF BINDING; 1
PROSITE; PS50092; TSP1; 1.
PROSITE; PS501208; VWFC_1; 1.
PROSITE; PS51208; VWFC_2; 1.
Coll official VWFC_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liliensiek B., Lin Z., Fotsis T., Schimanski M., Bierhaus
Kanitz M., Kauffmann G., Schweigerer L., Ziegler R., Nawro
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF000137; AAB66596.1; -; mRNA.
EMBL; AF309555; AAG30290.1; -; Genomic_DNA
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VWFC.
TSP type-1.
TSP type-1.
CTCK.
Heparin-binding Heparinarity.
By similarity.
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                                                                                                                                                                                                                                         Connective tissue
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Best Local S
Matches 169
                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Connective tissue growth factor precursor
Name=CTGF; Synonyms=CCN2;
sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                            "Purification and characterization of novel heparin-binding grounds in uterine secretory fluids. Identification as heparin-regulated Mr 10,000 forms of connective tissue growth factor."; J. Biol. Chem. 272:20275-20282(1997).
                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97390475; PubMed=9242708; DOI=10.1074/jbc.
Brigstock D.R., Steffen C.L., Kim G.Y., Vegunta R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
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98.3%;
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CV -> YI (in Ref. 1).

CDEP -> SRDE (in Ref. 1).

P -> L (in Ref. 1).

L -> Q (in Ref. 1).

C -> Y (in Ref. 1).

B -> Q (in Ref. 1).

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neria; Cetartiodactyla; Suina; Suida
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.K., Diehl J.R.,
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Best Local S
Matches 167
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InterPro; IPR006207; Cys_knot.
InterPro; IPR006207; Cys_knot.
InterPro; IPR012395; IGFBP_CNN.
InterPro; IPR000867; IGFBP_Like.
InterPro; IPR000867; TSP1__II.
InterPro; IPR001007; VWF_C.
INTERPRO; IPR001007; VWF_C.
INTERPRO; IPR001007; VWF_II.
INTERPRO; IPR001007; IGFBP; 1.
INTERPRO; I
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PROSITE; PS(
Cell adhesi(
Signal.
Signal.
CHAIN
CHAIN
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                                          Connective tissue growth factor precursor.
Name=Ctgf; Synonyms=Ccn2;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalla; Eutheria; Euarchontoglires; Glires;
Muroidea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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DOMAIN
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
10-MAY-2005 (Rel. 47, Last annotation
                                                                                                                                                                                                                                                     CIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
 NUCLEOTIDE SEQUENCE.
MEDLINE=20145935; PubMed=10679821;
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; pS01225; CTCK_2; 1.
; pS00222; IGF BINDING; 1.
; pS50092; TSPI; 1.
; pS01208; VWFC_1; 1.
; pS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                                                           TTTLPVEFKCPDGEVMKKSMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
                                                                                                                                                                                                                                                                                                                                                                            TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
                                                                                                                                                                                                                                                                                                                                                                                                                MVRPCEADLEENIKKGKKCIRTPKISKPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALAAYRLEDTFGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNAFCRLEKQSRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
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97.1%;
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TSP type-1.
CTCK.
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(on update)
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3.3e-79;
1es 1;
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"Rattus norvegicus connective tissue growth factor.";

RI Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

C: FUNCTION: Major connective tissue mitoattractant secreted by consecular endothelial cells. Promotes proliferation and differentiation of chondrocytes (By similarity). Mediates heparince and divalent cation-dependent cell adhesion in many cell types chocked and divalent cation-dependent cell adhesion in many cell types and divalent cation-dependent cell adhesion in many cell types cells (By similarity). Enhances fibroblasts, endothelial and epithelial cells (By similarity).

C: SUNCELLULAR LOCATION: Secreted.

C: SUNCELLULAR LOCATION: Secreted.

C: SUNTIARITY: Contains 1 CTCK (C-terminal cystine knot-like) domain.

C: SIMILARITY: Contains 1 TSP type-1 domain.

C: SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                        Pfam; PF00007; Cys_knot; 1.
Pfam; PF00009; TGFBP; 1.
Pfam; PF00009; TSP_1; 1.
Pfam; PF00009; TWC; 1.
Pfam; PF00009; VWC; 1.
Pfam; PF00009; VWC; 1.
SMART; SM00121; CT; 1.
SMART; SM00121; VWC; 1.
SMART; SM00121; VWC; 1.
PROSITE; PS00125; CTCK_1; 1.
PROSITE; PS0125; CTCK_2; 1.
PROSITE; PS00125; TSP1; 1.
PROSITE; PS00125; TSP1; 1.
PROSITE; PS00125; TSP1; 1.
PROSITE; PS00125; TSP1; 1.
PROSITE; PS001208; VWFC_1; 1.
PROSITE; PS001208; VWFC_1; 1.
PROSITE; PS001208; VWFC_1; 1.
CHAIN
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu J., Smock S.L., Safadi F.F., Rosenzwe Marks S.C. Jr., Owen T.A., Popoff S.N.; "Cloning the full-length cDNA for rat co implications for skeletal development.";
                                                                                                                                                                                                  Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse as long as its content is in no way modified and this s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
Tezuka K., Tamatani T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOI=10.1002/(SICI)1097-4644(20000401)77:1<103::AID-JCB11>3.0.CO;2-G;
Xu J., Smock S.L., Safadi F.F., Rosenzweig A.B., Odgren P.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ensembl; ENSRNOG00000015036; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000884; InterPro; IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR012395; InterPro; IPR000867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF120275;
AB023068;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; IPR006208; Cys_knot.
; IPR006207; Cys_knot.
; IPR002395; IGFBE CNN.
; IPR000867; IGFBE like.
; IPR000884; TSP1.
; IPR000087; VWE C.
; IPR001007; VWE C.
94
347
                           DNA
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BAA82125.1; -;
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              synthesis;
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           Connective tissue connective tissue connective tissue connective tissue connective tissue connective type-1.

TSP type-1.

CTCK.

CTCK.

Heparin-binding (B)

By similarity.

By similarity.
                                                                                                                                                                                                  Potential.
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    CFBE1A19766B7B16 CRC64;
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                                                                                                                  similarity).
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RROCCOSSIBET TACE
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Best Local Sim
Matches 165;
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Best Local
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                                                           CTGF MOUSE STANDARD; PRT; 348 AA.

P29268; Q922U0;

01-DEC-1992 (Rel. 24, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

10-MAY-2005 (Rel. 41, Last sequence update)

Connective tissue growth factor precursor (FISP-12 p)

Connective tissue growth factor precursor (FISP-12 p)

(Hypertrophic chondrocyte-specific protein 24).

Name=Ctgf; Synonyms-Ccn2, Fisp12, Hcs24;

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Connective Tissue Growth Related Gene.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
EMBL; AY596447; AAT08023.1; -; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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NUCLEOTIDE SEQUENCE
                                    Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTLPVEFKCPDGEIMKKNWMFIKTCACHYNCPGDNDIFESLYYRKWYGDMA 347
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Last annotation update)
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Pred. No. 6.3e-79;
5; Mismatches 2
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Pred. No. 6
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. 6.3e-79;
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                                                    Rodentia;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Cararinci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rodriguez A.C., Grimwood J., Schento V., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
T. Tand mouse cDNA sequences.";
T. Proc. Natl Acad S.c.i II s.A. 00.16409-16601/2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RX MEDLINE-99182484; PubMed=10082563;
RA Babic A.M., Chen C.-C., Lau L.F.;
RA Babic A.M., Chen C.-C., Lau L.F.;
RY "Fisp12/mouse connective tissue growth factor mediates endothelial rell adhesion and migration through integrin alphavbeta3, promotes rell adhesion and migration through integrin alphavbeta3, promotes rell adhesion and migration through integrin alphavbeta3, promotes rell adhesis in vivo.";
RY mol. Cell. Biol. 19:2958-2966(1999).
RY Mol. Cell. Biol. 19:2958-2966(1999).
RY Mol. Cell. Biol. 19:2958-2966(1999).
CC vascular endothelial cells. Promotes proliferation and differentiation of chondrocytes (By similarity). Mediates heparincy and divalent cation-dependent cell adhesion in many cell types and divalent cation-dependent cell adhesion in many cell types including fibroblasts, myofibroblasts, endothelial and epithelial cells (By similarity). Enhances fibroblast growth factor-induced DNA synthesis (By similarity).
CC DNA synthesis (By similarity).
CC -1- SUBCELULAR LOCATION: Found in the extracellular matrix and as a control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
MEDLINE=91229699; PubMed=2029337;
MEDLINE=91229699; PubMed=202999; PubMed=202937;
MEDLINE=91229699; PubMed=202999; PubMed=2029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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"Structure, mapping, and expression of fisp-12, &
inducible gene encoding a secreted cysteine-rich
Cell Growth Differ. 2:225-233(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91363290; PubMed=1888698;
This Swiss-Prot
between the Swi
the European Bio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97327410; PubMed=9184077; DOI=10.1006/excr.1997.3548;
Kireeva M.L., Latinkic B.V., Kolesnikova T.V., Chen C.-C., Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION
                                                                                                                                                                                                                                                                       soluble form.

ITISSUE SPECIFICITY: Testis, spleen, kidney
(lowest level in testis and highest in lun
INDUCTION: By growth factors.
INDUCTION: By growth factors.
ISIMILARITY: Contains 1 CTCK (C-terminal cy
ISIMILARITY: Contains 1 IGFBP domain.
ISIMILARITY: Contains 1 TSP type-1 domain.
SIMILARITY: Contains 1 VWPC domain.
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       Swiss Institute of Bioinf
Bioinformatics Institute.
entry is copyright. It is produced through a collaboration iss Institute of Bioinformatics and the EMBL outstation oinformatics Institute. There are no restrictions on its
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regulated by
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in lung).
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a growth factor-
h protein.";
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SMO041,
SMO012; IB,
SMO012; IB,
SMO0121; VWC; 1.

L; SM00214; VWC; 1.

L; SM00214; VWC; 1.

SITE; PS01125; CTCK 1; 1.
SITE; PS01225; CTCK 2; 1.

SITE; PS01225; CTCK 2; 1.

AOSITE; PS00222; IGF BIDING; 1.

AOSITE; PS00222; IGF SIDING; 1.

PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS01208; VWFC 1; 1.
Cell adhesion; DNA synthesis; E'
SIGNAL 1 25
SIGNAL 1 25
SIGNAL 1 99
FT DOMAIN 197 242
PT DOMAIN 197 242
PT DOMAIN 197 242
PT DOMAIN 197 242
PT DOMAIN 255 329
FT DISULFID 255
PT DISULFID 272
PT DISULFID 283
FT DISULFID 283
FT DISULFID 283
FT DISULFID 296
CONFLICT 1'
SEQUENCE 3

"CONFLICT 1'
                                                                                                                                                                                                                           Matches
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EMBL; M80263; AAA73135.1; -; mRNA.

EMBL; BC006783; AA40578.

EMBL; BC006783; AA40578.

ENBL; BC006783; AA40578.

ENBL; BC006783; AA40578.

ENBRUSG0000019997; Mus muscu.

MG; MG1:95537; Ctgf.

GO; GO:0005578; C:extracellular matrix

GO; GO:0005575; C:extracellular space;

GO; GO:0005575; F:heparin binding; IDA

GO; GO:0005178; F:integrin binding; IDA

GO; GO:0001525; P:angiogenesis; IDA

GO; GO:0001525; P:cartilage condensati

GO; GO:0001502; P:cell differentiation;

GO; GO:0001503; P:cell migration; IDA

GO; GO:0007160; P:cell-matrix adhesion

GO; GO:0008540; P:integrin-mediated sig

GO; GO:0001503; P:integrin-mediated sig

GO; GO:0001503; P:ossification; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00007; CyB_knot; 1.
Pfam; PF000219; IGFBP; 1.
Pfam; PF00093; TSP_1; 1.
Pfam; PF00093; VWC; 1.
PIRSP; PIRSF036495; IGFBP_rP_CNN; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM001214; VWC; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006208; Cys knot.
InterPro; IPR006207; Cys knot C.
InterPro; IPR012395; IGFBP CNN.
InterPro; IPR000867; IGFBP like.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF C.
Pfam; PF00007; Cys knot; 1.
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GO:0005201; F:heparin binding; IDA.
GO:0005178; F:integrin binding; IDA.
GO:0005178; F:enricerin binding; IDA.
GO:0001525; P:angiogenesis; IDA.
GO:0001502; P:cartilage condensation; IDA.
GO:0016477; P:cell differentiation; IDA.
GO:00016477; P:cell migration; IDA.
GO:0007150; P:cell-matrix adhesion; IDA.
GO:0007150; P:cell-matrix adhesion; IDA.
GO:000753; P:integrin-mediated signaling pathway; IDA.
GO:0001503; P:ossification; IMP.
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M70642; AAA37628.1; -; mRNA.
M80263; AAA73135.1; -; mRNA.
                                            237
                                                                                                                                      177
                                                                                                                                                                                                                             165;
  121
                                                                                    61
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENSMUSG00000019997; Mus musculus.
                                                                      MVRPCEADLBENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                         ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                                                                                    ALAAYRLEDTFGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNTFCRLEKQSRLC
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                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  extracellular matrix (sensu Metazoa); IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthesis; Extracellular matrix;
                                                                                                                                                                                                                                                97.7%;
95.9%;
                                                                                                                                                                                                                                                                                                                                     By similarity.
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                                                                                                                                                                                                                                                Score 934;
Pred. No. 6
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                                                                                                                                                                                                                                                                                                                    4D7B6D9089174049
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                    6.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue
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Best Local S
Matches 164
                                                                                                                                                                            PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF BINDING; 1
PROSITE; PS50092; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                    Pfam; PF00007; Cys knot; 1
Pfam; PF00019; IGFBP; 1.
Pfam; PF000090; TSP 1; 1.
Pfam; PF000093; VWC; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00121; IB; 1.
SMART; SM00214; VWC; 1.
                                                                                                                  Signal.
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NÜCLEOTIDE SEQUENCE.
MEDLINE=22984509; PubMed=14623326; DOI=10.1016/j.bbrc.2003.10.061;
Gygi D., Zumstein P., Grossenbacher D., Altwegg L., Luscher T.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
10-MBX-2005 (TrEMBLrel. 30, Last annotation update)
10-MBX-2005 (TrEMBLrel. 30, Last annotation update)
Connective tissue growth factor precursor (Connective factor/hypertrophic chondrocyte-specific protein 24).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
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28 CHICK

Q98TQ8_CHICK PRELIMINARY;

Q98TQ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22559415; PubMed=12674494; DOI=10.1515/BC.2003.001; Mukudai Y., Kubota S., Takigawa M.; "Conserved repressive regulation of connective tissue growt factor/hypertrophic chondrocyte-specific gene 24 (ctgf/hcs2 by different elements and factors among vertebrate species.
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000867; Insl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0005520; F:insulin-like growth factor b
GO; GO:0001558; P:regulation of cell growth; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ298335; CAC33438.1; -; mRNA.
EMBL; AF463517; AAL68834.1; -; mRNA.
Ensembl; ENSGALG00000002909; Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by different elements and factors Biol. Chem. 384:1-9(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Human connective tissue growth factor expressed is a non-mitogenic inhibitor of apoptosis."; Biochem. Biophys. Res. Commun. 311:685-690(2003).
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Gehring H.;
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
Pfam; PF00007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
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                                                           164;
                                                                         Similarity
ALAAYRLEDTYGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNAFCRLEKQSRLC
              ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
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22
344 AA;
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344
37499
                                                                      96.8%;
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                                                                                                                  Potential.
connective tissue (
69E639AF69BF1D00
                                                        Score 925; DB 2;
Pred. No. 4.3e-78;
5; Mismatches 3
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                                                                                                                       growth factor CRC64;
                                                                                      Length 344;
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                                                           Indels
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 232
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RESULT 12

OA2607 XENLA
OA2607 XENLA
OA2607 XENLA
OA2607 O1-JAN-1
DT 01-JAN-1
DT 01-FEB-2
DE CONNECTION
CO XENOPOOLI
OX XENOPOOLI

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Q505L5 XENLA PRELIMINARY; AC Q505L5;
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                                                                                     RESULT 13
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Best Local S
Matches 156
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InterPro; IPRO06207; Cys knot.
InterPro; IPRO06207; Cys knot.
InterPro; IPRO00867; Insl_gro_fac_pr.
InterPro; IPRO0084; TSP1.
InterPro; IPRO01007; VWF_C.
Pfam; PPO0209; IGFBP; 1.
Pfam; PPO0209; TSP_1; 1.
Pfam; PPO0093; VWC; 1.
SMART; SM000041; CT; 1.
SMART; SM000121; IB; 1.
SMART; SM000209; TSP1; 1.
SMART; SM00214; VWC; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01128; CTCK_2; 1.
PROSITE; PS01285; CTCK_2; 1.
PROSITE; PS01208; VWFC_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U43524; AAB67639.1; -; mRNA.
EMBL; U43523; AAB67638.1; -; Genomic DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0005520; F:insulin-like growth factor binding; IEA.
GO; GO:0005589; P:regulation of cell growth; IEA.
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Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ALAAYRLEDTFGPDDTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
                                                                                                                                                                                                         TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKNYGDMA 172
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                                                                                                                                                                           TATLPVEFKCPDGEVMKKNIMFIKTCACHFNCPGDNDIFEAMYYRKMYGDMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 898; DB 2;
Pred. No. 1.4e-75;
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                                PRT;
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
RA Rahby J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mitting M., Wadan A., Krzywinski M.I., Skalaka U., Smallus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
"To The Company of the Property of the Prop
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 156
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
Ctgf protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=ctgt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S., Gerhard D.S.;
Submitted (MAY-2005) to the
EMBL; BC094492; AAH94492.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissuE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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292
                                                              121
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                                                                                                                                                                                                                                                                 172
                                                                                                                                                                                                                                                                                                                                                                                                      156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natl. Acad.
                                                                                                                                                                       61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                                                   μ
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
TATLPVEFKCPDGEVMKKNIMMFIKTCACHFNCPGDNDIFEAMYYKKNYGDMA
                                                           TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                                                                                MVRPCEADLEENIKKGKKCIRTPKISKPVKFEFSGCTSVKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                 ALPAFRMEETYGPDPSLIRANCLVQTTEWSACSKTCGMGISTRVTNDNEHCRLEKQSRLC
                                                                                                                                                                                                                                                                                                           ALAAYRLBDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerhard D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94492.1; -; mRNA.
37879 MW; BF448D73C7774FD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus.
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31,
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                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.46
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 868
                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               띪
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 343;
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; Pipidae;
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RESULT 14
OSBKN7 XENTR
ID QSBKN7_XENTR PRELIMINARY;
AC QSBKN7;
DT 10-MAY-2005 (TrEMBLrel. 30,

Created)

PRT;

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                 A Klein S., Gerhard D.S.;

A Klein S., Gerhard D.S.;

EMBL; BCO91005; AAH91005.1; -; mRNA.

R Interpro; IPR006208; Cys_knot.

RR Interpro; IPR006208; Cys_knot C.

RINTERPro; IPR002867; INSI gro_fac_pr.

Interpro; IPR000867; InsI gro_fac_pr.

Interpro; IPR000867; InsI gro_fac_pr.

RINTERPRO; IPR000884; TSP1.

RPfam; PF00007; Cys_knot; 1.

RPfam; PF00007; Cys_knot; 1.

RPfam; PF00099; TSP1; 1.

RR Pfam; PF00099; TSP1; 1.

RR Pfam; PF00099; TSP1; 1.

RR Pfam; PF00099; TSP1; 1.

RR SMART; SM00121; III; 1.

RR PGASITE; SM00121; VWC; 1.

RR SMART; SM00121; VWC; 1.

RR SMART; SM00214; VWC; 1.

RR SMART; SM00214; VWC; 1.

RR SMART; SM00221; IGF BINDING; 1.

RR PROSITE; PS01225; CTCK 1; 1.

RR PROSITE; PS01226; VWFC_1; 1.

RR PROSITE; PS01226; VWFC_2; 1.

RR PROSITE; PS01208; VWFC_2; 1.
                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                     Matches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
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   232
                                                                                                                            172
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                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                         MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
      MVRPCEADLEENIKKGKKCIRTPKISKPVKFEISGCTSVKTYRAKFCGVCTDGRCCTPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences.";
1. Acad. Sci. U.S.A. 99:16899-16903(2002).
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(TrEMBLrel. 30, Last annotation
                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                  93.5%;
                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                  Score 894; DB
Pred. No. 3.4e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
                                                                                                                                                                                                                                        DB 2,
3.4e-75;
5;
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Best Local S
Matches 157
                                                                                                                                                                                                                   InterPro; IPR006208; Cys knot.
InterPro; IPR006207; Cys knot.
InterPro; IPR006207; Cys knot.
InterPro; IPR000867; INSI_gro_fac_pr.
InterPro; IPR000884; TSP1.
InterPro; IPR000884; TSP1.
InterPro; IPR00107; VWF C.
Pfam; PF00007; Cys knot; 1.
Pfam; PF00009; TSP 1; 1.
Pfam; PF000093; VWC; 1.
SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00214; VWC; 1.
SMART; SM00214; VWC; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS01285; CTCK 2; 1.
PROSITE; PS01285; CTCK 2; 1.
PROSITE; PS01202; IGF BINDING; 1.
PROSITE; PS01208; VWFC 1; UNKNOWN_1.
PROSITE; PS01208; VWFC 2; 1.
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80 NOTVI
09PT80_1
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

TISSUE=Forelimb blastema;

TISSUE=Forelimb blastema;

TISSUE=Forelimb blastema;

TISSUE=Forelimb blastema;

TISSUE=Forelimb blastenal cells.";

TISSUE=Forelimb blastenal cells.";

Gene 222:119-124(1998).
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GO; GO:0005520; F:insulin-like growth factor binding;
GO; GO:0005520; F:insulin-like growth factor binding;
GO; GO:0001558; P:regulation of cell growth; IBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Notophthalmus viridescens (Eastern newt) (Triturus viridescens)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=ctgt;
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                           121
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                                                                                                                                                                  157;
                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTVI PRELIMINARY;
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
                                                      MVRPCEADLEENIKKGKKCIRTPKISKPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR
                                                                                                           ALAVYROEETYGPDSSLMRANCLVOTTEWSACSKTCGMGISTRVTNDNEMCRLEKOSRLC
                                                                                                                          ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
                        TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blastema;
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                                                                                                                                                                              93.4%;

    Created)
    Last sequence update)
    Last annotation updat
    h factor.

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                                                                                                                                                                 Score 893; Db z; L
Pred. No. 4.2e-75;
                                                                                                                                                                                                                       3B7E2399F27672C1 CRC64;
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IEA.
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                                                                                                                                                                    Gaps
                                                                                    120
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Search completed: January 9, 2006, 11:19:08 Job time : 162 secs This Page Blank (uspto)

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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
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Copyright (c) 1993 - 2006 Compugen Ltd.
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ATTORNEY/AGENT INFORMATION: NAME: MULLINS, J.G. REGISTRATION NUMBER: 33,073 REFERENCE/DOCKET NUMBER: 325800-442 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700 TELEPHONE: 201-994-174 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 348 AMINO ACIDS TYPE: AMINO ACID STRANDEDNESS: TOPOLOGY: LINEAR	ARM ROAD M: NCH DISKETT NS-DOS (FECT 5.1 ATTA: US/08/468 1995	RESULT 1 US-08-468-847B-14 ; Sequence 14, Application US/08468847B ; Patent No. 5780263 ; GENERAL INFORMATION: APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20 ; CORRESPONDENCE ADDRESS: ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, NUMBERSEE: CARELLA, BYRNE, BAIN, GILFILIAN,	28 546.5 57.2 351 2 US-09-495-448A-34 29 519 54.3 357 2 US-09-253-316-25 30 519 54.3 357 2 US-09-253-316-25 31 487.5 51.0 379 1 US-08-468-847B-11 32 487.5 51.0 379 2 US-09-142-569-4 34 485.5 50.8 381 2 US-09-142-569-4 35 485.5 50.8 381 2 US-09-142-569-4 36 485.5 50.8 381 2 US-09-495-448A-2 37 479.5 50.2 375 1 US-08-468-847B-13 38 479.5 50.2 375 1 US-08-468-847B-13 39 469.5 49.1 374 1 US-08-468-847B-12 40 468.5 49.0 375 1 US-08-468-847B-12 41 423 44 2 345 2 US-09-182-145-12 42 43 40 372 2 US-09-182-145-33 43 40 42 33 2 US-09-182-145-33 44 40 42.3 339 2 US-09-182-145-33
	·		Sequence 17, Appl Sequence 17, Appl Sequence 25, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 33, Appl Sequence 12, Appli Sequence 12, Appli Sequence 11, Appl Sequence 12, Appli Sequence 11, Appli Sequence 12, Appli Sequence 33, Appli Sequence 36, Appli

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RESULT 3
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                                                                                                                                                                                                                                                                                  Query Match
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Matches 172; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: lin-
OLECUT
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
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COMPUTER READABLE FORM:
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STREET: 422
CITY: La Jolla
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APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Wetherell, Jr. Ph.D., REGISTRATION NUMBER: 31,678 REFERENCE/DOCKET NUMBER: PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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ZIP: 92037
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                                                                          TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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                                                                                                                                  MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
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                                                       TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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                                                                                                                                                                                                                                                                                  100.0%; Score 956; DB 1; Length 349; llarity 100.0%; Pred. No. 1.9e-83; Conservative 0; Mismatches 0; Indels
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US-08-386-680-2

GENERAL INFORMATION:

APPLICANT: Grotendorst, Gary R.

APPLICANT: Bradham Jr., Douglas M.,

APPLICANT: Bradham Jr., Douglas M.,

APPLICANT: Bradham Jr., Douglas M.,

TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH

TITLE OF SEQUENCES:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSES: Spensley Horn Jubas & Lubitz

STREET: 4225 Executive Square, Suite 1400

GROWTH

FACTOR

La Jolla

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                                       US-08-459-717-2
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Sequence 2, Application US/08459717 Patent No. 5770209
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
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APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John
REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
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                                                                                                                                   TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                                                                                                                                                                                                             ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237
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4225 Executive Square, Suite 1400
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HOLECULE TYPE: protein
US-08-459-717-2
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/459,717
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/752,427
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph. D., John W.
REGISTRATION NUMBER: 31.678
REFERRNCE/DOCKET NUMBER: PD-1294
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08712302
Patent No. 5783187
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Best Local Similarity
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,302
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                              APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OP INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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LENGTH: 349 amino acids
TYPE: amino acid
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MEDIUM TYPE: Ploppy
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STREET: %***
CITY: La Jolla
------E: CA
PRIOR APPLICATION DATA:
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al Similarity 100.0%;
172; Conservative 0;
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                                                                                                                                                                                                                                                                             4225 Executive Square, Suite 1400
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Pred. No. 1.9e-83;
0; Mismatches 0;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-712-302-2
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Best Local Similarity 100.0%;
Matches 172; Conservative 0
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN RAPPLICATION NUMBER: US/08/880,031
APPLICATION NUMBER: US/08/880,031
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
APPLICATION NUMBER: US/08/167,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAMB: Wetherell, Jr. Ph.D., J
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
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NAME: Wetherell, Jr. Ph.D.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD
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TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
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CITY: La Jolla
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 MYRPCEADLBENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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                                                 PD-1294
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Pred. No. 1.9e-83
); Mismatches 0
                                                                                       John
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CURRENT APPLICATION NUMBER: US/09/054,368
CURRENT FILING DATE: 1998-04-02
EARLIER APPLICATION NUMBER: 08/386,680
EARLIER FILING DATE: 1995-02-10
EARLIER FILING DATE: 1995-02-17
EARLIER FILING DATE: 1995-06-02
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER APPLICATION NUMBER: 08/67,628
EARLIER FILING DATE: 1993-12-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 2
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                                                    RESULT 8
US-09-097-179-2
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Sequence 2, Application US/09097179 Patent No. 6149916 GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: University of South Florida
APPLICANT: Grotendorst, Gazy R.
APPLICANT: Bradham, Jr., Douglass M.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 07414/003005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 349
TYPE: PRT
ORGANISM: Homo Sapiens
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    349 amino acids
amino acid
    CY: linear

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                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 956; DB 2;
100.0%; Pred. No. 1.9e-83;
tive 0; Mismatches 0;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                    Best Local Similarity Matches 172; Conserv
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. ph.D., J.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,179
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4
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                                121
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                                                                                                    61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
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                     TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                                                       MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
                                                                                                                                               ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC
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4225 Executive Square, Suite 1400
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Pred. No. 1.9e-83;
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                                                                                                                                                                                                                                                         Length 349;
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WS-09-054-274-2
US-09-054-274-2
; Sequence 2, Application US/09054274
; Patent No. 6150101
; Patent No. 6150101
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Bradham, Jr., Douglass M.
; APPLICANT: Bradham, Jr., Douglass M.
; APPLICANT: Bradham, Jr., Douglass M.
; TITLE OF INVENTION: HAT ALTERS CONNECTIVE TISSUE GROWTH
; TITLE OF INVENTION: FACTOR EXPRESSION (Amended)
; FILE REFERENCE: 07414/003004
; CURRENT APPLICATION NUMBER: US/09/054,274
; CURRENT FILING DATE: 1998-04-02

120 297 237

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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 349
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-054-274-2
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US-09-080-715-2
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Patent No. 6190884
GENERAL INFORMATION:
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EARLIER FILING DATE: 1995-02-10
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER FILING DATE: 1995-06-02
EARLIER FILING DATE: 1995-06-02
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER FILING DATE: 1993-12-14
NUMBER OF SEO ID NOS: 9
                                                                                                         FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGRERICEJ/DOCKET NUMBER: 31,678
REGRERICEJ/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
                                                                         TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
NUMBER OF SEQUENCES: 2
            SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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CITY: La Jolla
STATE: CA
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TOPOLOGY:
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
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4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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Pred. No. 1.9e-83;
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APPLICANT: University of South Florida
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham, Jr., Douglass M.
APPLICANT: Bradham, Jr., Douglass M.
TITLE OF INVENTION: CHARACTERIZED BY A CELL PROLIFERATIVE
TITLE OF INVENTION: CHARACTERIZED BY A CELL PROLIFERATIVE
TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE
TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE
TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE
TITLE OF INVENTION: TISSUE GROWTH FACTOR (Amended)
FILE REFERENCE: 07444/003002
CURRENT APPLICATION NUMBER: US/09/056,704
CURRENT FILING DATE: 1998-03-03
EARLIER APPLICATION NUMBER: 08/986,680
EARLIER FILING DATE: 1995-02-10
EARLIER FILING DATE: 1995-06-02
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER FILING DATE: 1993-12-14
NUMBER OF SEQ ID NOS: 9
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Best Local Similarity
Matches 172; Conserv
Sequence 4, Application US/09292036
Patent No. 6358741
GENERAL INFORMATION:
APPLICANT: FIBROGEN, INC
APPLICANT: SCHMIDT, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
LENGTH: 349
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Patent No. 6232064
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                           h 100.0%; Score 956; DB 2; Similarity 100.0%; Pred. No. 1.9e-83; 72; Conservative 0; Mismatches 0;
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Pred. No. 1.9e-83;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/253,316
CURRENT FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: US 60/075,300
EARLIER FILING DATE: 1998-02-20
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH
FILE REFERENCE: 97-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: PRT
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TYPE: PRT
ORGANISM: Homo sapiens
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1es 172; Conservative
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                TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Pred. No. 1.9e-83;
                                                                                                                                                                         Score 956; DB 2;
Pred. No. 1.9e-83;
Mismatches 0;
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                                                                                                                                                                                                      Length 349;
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                                                                                         Sequence 2, Application US/09461688 Patent No. 6492129
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Lau, Lester F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 172;
            APPLICANT: Grotendorst, Gary R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
TITLE OF INVENTION: FRAGMENTS AND METHODS AND USES
FILE REFERENCE: FIBRO1140-2
CURRENT APPLICATION NUMBER: US/09/461,688
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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STATE: Illinois
                                                                                                                                                                                                                                                                TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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100.0%; Pred. No. 1.9e-83;
rative 0; Mismatches 0;
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Tower, 233
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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                                                                                                         Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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(without alignments)
624.927 Million cell updates/sec
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Result

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US-11-149-564-26	4	-10-955-860A-	- 1	-10	•	US-10-858-186-2	5-889-	US-10-721-336-3	27-604-	•	US-10-464-368-55	US-10-428-487-44	US-10-338-587A-2	US-10-182-432-8	US-10-131-985-7	US-10-394-015-4	US-10-315-568-2	US-10-245-977-2	US-10-205-823-78	US-10-171-311-46	US-10-060-036-173	US-10-053-753-8	US-10-011-859-26	US-10-101-040-4	US-09-853-625B-14	US-10-658-856-4	ID
Sequence 26, Appl	e 78,	, -	14,	e 7,	8,	Sequence 2, Appli	e 60,	Sequence 3, Appli	Sequence 14, Appl	Sequence 2, Appli	e 55,	Sequence 44, Appl	e 2,	е в,	7,	Sequence 4, Appli	۵	•	Sequence 78, Appl	-	e 173	Sequence 8, Appli	e 26,	•	Sequence 14, Appl	Sequence 4, Appli	Description

5	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30	29	0
915	915	934	934	934	934	934	934	934	934	934	934	934	934	937	938	938	0
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US-10-101-040-2	US-10-080-173-2	US-10-627-604-15	US-10-902-895-6	US-10-627-604-15	US-10-464-368-54	US-10-182-432-6	US-10-245-977-8	US-10-053-753-6	US-10-101-040-3	US-09-853-625B-15	US-10-464-368-56	US-10-390-986-2	US-10-245-977-7	US-10-245-977-6	US-10-245-977-5	US-10-617-316-163	0 10 10 10 10 10 10 10 10 10 10 10 10 10
Sequence 2,	Sequence 2,	Sequence 15,	Sequence 6,	Sequence 15,		Sequence 6,	Sequence 8,	Sequence 6,	Sequence 3,	Sequence 15,	Sequence 56,	Sequence 2,	Sequence 7,	Sequence 6,	Sequence 5,	Sequence 163	
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ALIGNMENTS

US-10-658-856-4

GENERAL INFORMATION:

Sequence 4, Application US/10658856 Publication No. US20040092450A1

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PRIOR APPLICATION NUMBER: US/09/461,646
PRIOR PILING DATE: 2003-09-09
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: US/09/461,646
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/112,241
PRIOR FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 172
TYPE: PRT
                                                                                                                  RESULT 2
US-09-853-625B-14
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Sequence 14, Application US/09853625B
Patent No. US20020049304A1
PATENT INFORMATION:
GENERAL INFORMATION: Gregg A. and Adams, Mark D.
APPLICANT: Hastings, Gregg A. and Adams, Mark D.
TITLE OF INVENTION: Human CCN-Like Growth Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 956; DB 4; Length 172; Best Local Similarity 100.0%; Pred. No. 8.4e-84; Matches 172; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Grotendorst, Gary
APPLICANT: Neff, Thomas
TITLE OF INVENTION: Connective Tissue Growth Factor Fragments and Methods and Uses Ti
FILE REFERENCE: FIBRO1130-2
CURRENT APPLICATION NUMBER: US/10/658,856
CURRENT FILING DATE: 2003-09-09
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NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:

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RESULT 3
US-10-101-040-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10101040 Publication No. US20020142353A1 GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: PIEROGEN, INC
APPLICANT: SCHMIDT, Brian
APPLICANT: ALLEN, Margaret
APPLICANT: SVERDBUP, Fran
APPLICANT: SVERDBUP, Fran
APPLICANT: CARMICHAEL, David
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS:
TITLE OF INVENTION: USE
FILE REFERENCE: FIERO1100-1
CURRENT APPLICATION NUMBER: US/10/101,040
CURRENT APPLICATION NUMBER: 09/292,036
PRIOR APPLICATION NUMBER: 09/292,036
PRIOR APPLICATION NUMBER: US 09/292,036
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYDE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD DERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/853,625B

FILING DATE: 14-May-2001

CLASSIFICATION: <UNknown>

PRIOR APPLICATION DATA:

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NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 348 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: <Unknown>
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
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CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
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; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo s
US-10-011-859-26
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Publication No. US20020147328A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/253,316

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-19

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/075,300

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-20

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 34 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS
FILE REFERENCE: 97-75
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298
                                                                                     238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR
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                                  TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
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RESULT 5
US-10-053-753-8
; Sequence 8, Application US/10053753
; Publication No. US20020150986A1
; GENERAL INFORMATION:

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US-10-060-036-173
Sequence 173
Publication US/10060036
Publication No. US20030073144A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 172; Conserv
                                                                 APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hepler, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATION DATA:

SOFTWARE: PatentIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/053,753

FILING DATE: 22-Jan-2002

CLASSIFICATION: <underwarion:

ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: "CTGF amino acid sequence'
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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100.0%; Pred. No. 1.8e-83;
ative 0; Mismatches 0;
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South Wacker Drive
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-46
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 173
SEQ ID NO 173
LENGTH: 349
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APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
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Publication No. US20030087270A1
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Best Local
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NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/335,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS,
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENTITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
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ORGANISM: Homo sapiens
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 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
                  TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKNYGDMA 172
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Kamatkar, Shubhangi
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Zhao, Xumei
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100.0%; Pred. No. 1.8e-83;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                   Score 956; DB 4;
Pred. No. 1.8e-83;
; Mismatches 0;
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US-10-205-823-78

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CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-08-25
PRIOR ELING DATE: 2001-08-25
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR PRIOR DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR APPLICATION NUMBER: 60/362,158
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Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                               Sequence 2, Application US/10245977 Publication No. US20030113816A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 78
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APPLICANT:
APPLICANT:
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               APPLICANT: Weitz, Stephen L
APPLICANT: Usinger, William R
APPLICANT: Usinger, William R
INTER OF INVENTION, METHODS OF ASSAYING CONNECTIVE
FILE REFERENCE: FP0812 US
CURRENT APPLICATION NUMBER: US/10/245,977
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/323,305
PRIOR FILING DATE: 2001-09-18
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APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
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NUMBER OF SEQ ID NOS: 8
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TYPE: PRT
ORGANISM: Homo sapiens
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Kamatkar, Shubhangi
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US-10-394-015-4

Sequence 4, Application US/10394015 Publication No. US20030180891A1 GENERAL INFORMATION:

APPLICANT: Young, Paul APPLICANT: Ruben, Ste

Steven M.

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; TYPE: PRT
; ORGANISM: Homo
US-10-245-977-2
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US-10-315-568-2
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Publication No. US20030180300A1
GENERAL INFORMATION:
APPLICANT: FibroGen, Inc.
APPLICANT: Grotendorst, Gary R.
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LENGTH: 349
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Best Local
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TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR FRAGMENTS AND METHODS AND USES FILE REFERENCE: FIBRO1140-3
CURRENT APPLICATION UNUMBER: US/10/315,568
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION UNUMBER: US 09/461,688
PRIOR APPLICATION NUMBER: US 60/112,240
PRIOR APPLICATION NUMBER: US 60/112,240
PRIOR FILING DATE: 1998-12-14
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Best Local Similarity
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ORGANISM: Homo sapiens
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TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
                                      TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Pred. No. 1.8e-83;
; Mismatches 0;
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Pred. No. 1.8e-83;
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APPLICANT: Dack, Kevin N
APPLICANT: Davies, Michael J
APPLICANT: Davies, Michael J
APPLICANT: Huggins, Jonathan P
APPLICANT: Huggins, Jonathan P
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: Occleston, Nicholas L
TITLS OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT APPLICATION NUMBER: US/10/131,985
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/726,295
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 9930768.8
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 7
LENGTH: 349
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; ORGANISM: Homo sapiens
US-10-394-015-4
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/ ORGANISM: Homo sapiens
US-10-131-985-7
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CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US/09/325,019
PRIOR FILING DATE: 1999-06-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/088,320
PRIOR FILING DATE: BARLIER FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
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Best Local Similarity
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    TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                                           MVR PCEADLEENI KKGKKCIRTPKI SKPIKPELSGCTSMKTYRAKFCGVCTDGRCCTPHR
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Pred. No. 1.8e-83;
); Mismatches 0;
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                                                                                                                                                NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn vers
SEQ ID NO 2
LENGTH: 349
TYPE: PRT
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                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 09/054,363
PRIOR FILING DATE: 1998-04-02
PRIOR PELICATION NUMBER: US 08/459,717
PRIOR PELICATION NUMBER: US 08/459,717
PRIOR APPLICATION NUMBER: US 08/386,680
PRIOR PILING DATE: 1995-02-10
PRIOR PELICATION NUMBER: US 08/167,628
PRIOR APPLICATION NUMBER: US 08/167,628
PRIOR APPLICATION NUMBER: US 08/167,628
PRIOR APPLICATION NUMBER: US 07/752,427
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Publication No. US20040002124A1
GENERAL INFORMATION:
APPLICANT: LAU, Lester F., YEUNG, Cho-Yau, and GREENSPAN, Jeffrey
TITLE OF INVENTION: CYR61 COMPOSITIONS AND METHODS
FILE REFERENCE: 214448/00029
CURRENT APPLICATION NUMBER: US/10/182,432
CURRENT FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 38
SOUTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 349
TYPE: DET
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Query Match 100.0%; Score 956; DB 4; Best Local Similarity 100.0%; Pred. No. 1.8e-83; Matches 172; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: THE UNIVERSITY OF SOUTH FLORIDA
APPLICANT: GROTENDORST, GATY R.
APPLICANT: BRADHAM, Douglass M.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
FILE REFERENCE: USF1100-15
                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1991-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/338,587A CURRENT FILING DATE: 2003-01-07
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GENERAL INCOMPALIAN:
APPLICANT: GERBER, HANG-PETER
APPLICANT: GERBER, HANG-PETER
TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM
FILE REFERENCE: 09800080-0103
CURRENT APPLICATION NUMBER: US/10/428,487
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/815,153
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PATENCIAN VET: 2.1
SEQ ID NO 44
LENGTH: 349
TYPE: BFT
ORGANISM: Homo sapiens
Search completed: January
Job time : 116 BecB
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US-10-428-487-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 956; DB 4; Length 349; Best Local Similarity 100.0%; Pred. No. 1.8e-83; Matches 172; Conservative 0; Mismatches 0; Indels
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November 2005

available for processing searches. generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now

applications make up the Published_Applications_Main databases. Newly published applications will appear in the Published_Applications_New databases: older published

Searches run against Amino Acid Published_Applications produce two sets of results, with the ex Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extension rapbm (Published_Applications_AA_Main) and rapbn (Published_ .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New). Applications AA New

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Title: Perfect score: Sequence:

Scoring table:

Minimum DB Maximum DB

3

protein 9

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Sequence 596, App
Sequence 28, Appl
Sequence 28, Appl
Sequence 24, Appl
Sequence 5, Appli
Sequence 6, Appli
Sequence 23, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 10, Appl
Sequence 11, Appl

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Post-processing: Minimum Match 0%
Maximum Match 10
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2 6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*
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US-11-067-121-14

US-10-821-234-1020

US-11-067-121-5

US-11-067-121-15

US-11-067-121-15

US-11-039-138-12

US-11-039-398-16

US-11-039-398-16

US-11-039-398-16

US-11-039-398-10

US-11-039-398-10

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US-11-039-157A-18

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Sequence 14, Appl Sequence 5, Appl: Sequence 5, Appl: Sequence 18, Appl Sequence 16, Appl Sequence 12, Appl Sequence 10, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 11, Appl Sequence 10, Appl Sequence 11, Appl Sequence 22, Appl Sequence 27, Appl Sequence 27,
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US-11-067-121-14

Sequence 14, Application US/11067121

Publication No. US20050261185A1

GENERAL INFORMATION:
APPLICANT: Martijn, Cecile
APPLICANT: Rondahl, Lena

TITLE OF INVENTION: THERAPEUTIC PROTEINS
FILE REFERENCE: 19809-002001

CURRENT APPLICATION NUMBER: US/11/067,121

CURRENT FILING DATE: 2004-02-25

PRIOR APPLICATION NUMBER: US 60/576,445

PRIOR APPLICATION NUMBER: US 0400489-1

PRIOR FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 20

SOPTWARE: FASUSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 349

TYPE: PRT

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US-10-821-234-1020
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                                                                 Sequence 1020, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
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Best Local :
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        APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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Similarity 100.0%; Pred. No. 1.3e-88;
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US-11-046-644-28

US-11-022-562-224

US-11-186-284-4

US-11-143-986-5

US-11-143-986-6

US-11-139-398-25

US-11-139-398-25

US-11-139-398-25

US-11-139-157A-13

US-11-109-157A-13

US-11-109-157A-13

US-11-109-157A-13

US-11-109-157A-13

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US-11-109-157A-13

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Regult No.

Score

956 956 934 925 848 432

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Gaps

120 237

Length Indels

148 103.5 103.5 103.5 103.5 103.5 102.2 102.2 102.9 102.9 102.9 102.9 102.9 102.9 102.9 102.9 102.9 102.9 103.5 103.5 104.5 105.5 106.6 10

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APPLICANT: Rondahl, Lena
APPLICANT: Rondahl, Lena
TITLE OF INVENTION: THERRAPEUTIC PROTEINS
FILE REFERENCE: 18909-002001
CURRENT APPLICATION NUMBER: US/11/067,121
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 60/576,445
PRIOR APPLICATION NUMBER: US 60/576,445
PRIOR FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: SE 0400489-1
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEO ID NOS: 20
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOPTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1020
SEQ ID NO 1020
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Best Local
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                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Methods for Diagnosis and
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 348
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 397
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297
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                                                                                   237 MVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR
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Similarity 95.9%;
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                                                                                                                                                                     ALAAYRLEDTEGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNTFCRLEKQSRLC 236
                                     TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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    TTTLPVEFKCPDGEIMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA
                                                                                                                                                                                                                                                           Conservative
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Pred. No. 2e-86;
5; Mismatches
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Pred. No. 1.5e-88;
                                                                                                                                                                                                                                                                                                   DB 7; Length 348;
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RESULT

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GENERAL INFORMATION:
APPLICANT: MATCHIN, Cecile
APPLICANT: MATCHIN, Lena
APPLICANT: ROMANH, Lena
ITILE OF INVENTION: THERAPEUTIC PROTEINS
FILE REFERENCE: 18909-002001
CURRENT APPLICATION UMBER: US/11/067,121
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 60/576,445
PRIOR FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: SE 0400489-1
PRIOR FILING DATE: 2004-02-27
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                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-11-067-121-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/11094519A
Publication No. US20050281810A1
GENERAL INFORMATION:
APPLICANT: BERNSTEIN, Jeanne
APPLICANT: LEVINE, Zurit
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0140P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 317
                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 15
                                                                                                                                                             Query Match 88.7%;
Best Local Similarity 99.3%;
Matches 151; Conservative
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CURRENT FILING DATE: 2005-03-31
CURRENT FILING DATE: US/09/695,293
PRIOR APPLICATION NUMBER: US/09/695,293
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: IL 132558
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEG ID NOS: 52
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                         LENGTH: 32
TYPE: PRT
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ORGANISM: Homo sapiens
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                                                                                                       NCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCI 80
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                     RTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKNM 140
                                                                                 DCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCI 230
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RTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKNM
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2004-02-27
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99.4%;
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                                                                                                                                                                 Score 848; DB 7;
Pred. No. 7.2e-78;
1; Mismatches 0
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Pred. No. 1.4e-85;
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                                                                                                                                                                                                        Length 322
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MFIKTCACHYNCPGDNDIFESLYYRKMYGDMA

172

MFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 322

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APPLICANT: BENSTEIN, Jeanne
APPLICANT: LEVINE, ZUTİL
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPI
FILE REFERENCE: 2786-0140P
CURRENT APPLICATION NUMBER: US/11/094,519A
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US/09/695,293
PRIOR APPLICATION NUMBER: US/09/695,293
PRIOR APPLICATION NUMBER: IL 132558
PRIOR APPLICATION NUMBER: IL 132558
PRIOR APPLICATION NUMBER: IL 132558
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 46
LENGTH: 74
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APPLICANT:
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APPLICANT: WACHARDE, COLIN K
APPLICANT: WOOD, WILLIAM
APPLICANT: WOOD, WILLIAM
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: 05/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/056974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                         Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                Gao, Wei-Qiang
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                                                                                                                                                                                                                                                               Stewart, Timothy A
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PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR PEPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR APPLICATION NUMBER: 60/059352
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                         SEQ ID NO 12
LENGTH: 1216
TYPE: PRT
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Matches
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PRIOR FILING DATE: 1997-09-17
PRIOR PELLATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: LEX-0221-USA
CURRENT APPLICATION NUMBER: US/11/039,398
CURRENT FILING DATE: 2005-01-20
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TITLE OF INVENTION: Novel Human Proteases and
TITLE OF INVENTION: Polynucleotides Encoding
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les 25; Conserv
                                                       894 PKPÍRRRCNOHPCSOPVWVÍBEWGÁCSRSCGKLGVOÍR----GIQCLLPLSNGTHKVMPA 949
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                                                                                                                                  h 10.8%;
Similarity 22.6%;
45; Conservative 24
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                                                                                                                                    ; Score 103.5; DB 7; ; Pred. No. 0.0061; 24; Mismatches 57;
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TYPE: PRT
ORGANISM: homo sapiens
US-11-039-398-8
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US-11-039-398-8
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                                      Sequence 16, Application US/11039398
Publication No. US20050267297A1
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
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Best Local (
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APPLICANT:
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PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT:
                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/039,398
CURRENT FILING DATE: 2005-01-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 10.8%; Score 103.5; DB 7; Local Similarity 22.6%; Pred. No. 0.0062; Cocal Similarity 24; Mismatches 57;
                                                                                                                                                                                                                                                                                     1060 M----CAAE-PCTGDRSVF 1073
                                                                                                                                                                                                                                                                                                                                                                      1000 NSLGHCEGDRPDTVQVCSLPACGGNHONSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059
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                                                                                                                                                                                                                                                                                                                         141 MFIKTCACHYNCPGDNDIF 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   894 PKPIRRRCNQHPCSQPVWVTEEWGACSRSCGKLGVQTR----GIQCLLPLSNGTHKVMPA 949
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Hu, Yi
Nepomnichy, Boris
Hu, Yi
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RESULT 11
US-11-039-398-20
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                                                                                                 ; ORGANISM: homo US-11-039-398-20
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CURRENT APPLICATION NUMBER: US/11/039,398
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR PILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                               NUMBER: FASTS
SOFTWARE: FASTS
SEQ ID NO 20
FENGTH: 1252
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SEQ ID NO 16
LENGTH: 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/11039398
Publication No. US20050267297A1
Query Match 10.8%;
Best Local Similarity 22.6%;
Matches 45; Conservative 2
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APPLICANT: Hu, Yi
TITLE OF INVENTION: Novel Human Proteases and
TITLE OF INVENTION: Polymucleotides Encoding the Same
TITLE REFERENCE: LEX-0221-USA
CURRENT APPLICATION NUMBER: US/11/039,398
CURRENT FILING DATE: 2005-01-20
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                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR PILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
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APPLICANT: Turner, C. Alexander
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
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                                                                                                                                                LENGTH: 12
TYPE: PRT
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nes 45; Conserv
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                                                                                                                                                                                                                         FastSEQ for Windows Version 4
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       Score 103.5; DB 7;
Pred. No. 0.0063;
24; Mismatches 57;
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24;

Indels

73;

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APPLICANT: Hu, Yi
TITLE OF INVENTION: Novel Human Proteases and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0221-USA
CURRENT APPLICATION NUMBER: US/11/039,398
CURRENT APPLICATION NUMBER: US/09/938,330
PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR PILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
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RESULT 13
US-11-039-398-10
US-11-039-398-10
; Sequence 10, Application US/11039398
; Publication No. US20050267297A1
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Best Local S
Matches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 1213
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APPLICANT:
APPLICANT:
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                          1060 TEPCTGDRSVF 1070
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                                                                                                                                                                                      149 HYNCPGDNDIF 159
                                                                                                                                                                                                                                                                                109 ------VCTDGRCCTPHRTTTLPV---EFKCPDGEVMKKN--MMFIKTCAC 148
                                                                                                                                                                                                                                                                                                                              950 KACAGDRPEARRPCLRVP---CPAQWRLGAWSQCSAT-----CGEGIQQRQVVCRTNA
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22.0%; Pred. No. 0.0087;
1tive 27; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 1213;
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TITLE OF INVENTION: Novel Human Proteases and TITLE OF INVENTION: Polynucleotides Encoding the FILE REFERENCE: LEX-0221-USA (CURRENT APPLICATION NUMBER: US/11/039,398); CURRENT FILING DATE: 2005-01-20 PRIOR APPLICATION NUMBER: US/09/938,330 PRIOR FILING DATE: 2001-08-22 PRIOR FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: US 60/227,104 PRIOR FILING DATE: 2000-08-22 PRIOR FILING DATE: 2000-08-22 PRIOR FILING DATE: 2000-09-19 NUMBER US 60/233,796 PRIOR FILING DATE: 2000-09-19 NUMBER OF SEQ ID NOS: 26 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/11039398; Publication No. US20050267297A1; GENERAL INFORMATION: APPLICANT: Friddle, Carl Johan; APPLICANT: Turner, C. Alexander Jr. APPLICANT: Walke, D. Wade; APPLICANT: Hilbun, Erin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Novel Human Proteases and TITLE OF INVENTION: Polynucleotides Encoding the TITLE REFERENCE: LEX-0221-USA CURRENT APPLICATION NUMBER: US/11/039,398 CURRENT FILING DATE: 2005-01-20 PRIOR APPLICATION NUMBER: US/09/938,330 PRIOR FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: US/0227,104 PRIOR APPLICATION NUMBER: US/0227,104 PRIOR APPLICATION NUMBER: US/0227,104 PRIOR PILING DATE: 2000-08-22 PRIOR PILING DATE: 2000-09-19 PRIOR FILING DATE: 2000-09-19 PRIOR FILING DATE: 2000-09-19 PRIOR FILING DATE: 2000-09-19
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APPLICANT: Friddle, (
APPLICANT: Turner, (
APPLICANT: Walke, D.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 1219
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nepomnichy, Boris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1060 TEPCTGDRSVF 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      894 PKPIRRRCNQHPCSQPVWVTEEWGACSRSCGKLGVQTR----GIQCLLPLSNGTHKVMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            950 KACAGDRPEARRPCLRVP---CPAQWRLGAWSQCSAT-----CGEGIQQRQVVCRTNA 999
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Turner, C. Alexander Jr.
Walke, D. Wade
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Nepomnichy, Boris
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Pred. No. 0.0087;
Pred. No. 6.0087;
Mismatches 6
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the

DB 7; Length 1219;

Indels

60;

Gaps

949

108

148

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APPLICANT: Nepomnichy, Boris
APPLICANT: Hu, Yi
INPLICANT: Hu, Yi
ITILE OF INVENTION: Novel Human Proteases and
ITILE OF INVENTION: Polynucleotides Encoding the Same
ITILE OF INVENTION NUMBER: US/11/039,398
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR PILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEG ID NOS: 26
PRIOR FILING DATE: 2000-09-19
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; ORGANISM: homo sapiens
US-11-039-398-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.7%; Score 102; DB 7; Length 1249; Best Local Similarity 22.0%; Pred. No. 0.0089; Matches 42; Conservative 27; Mismatches 62; Indels 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/11039398 Publication No. US20050267297A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.7%; Score 102; DB 7; Length 1232; Best Local Similarity 22.0%; Pred. No. 0.0088; Matches 42; Conservative 27; Mismatches 62; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059
                                                                                   1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059
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149 HYNCPGDNDIF 159
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Search completed: January 9, 2006, 11:31:22 Job time : 28 secs